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WATERMAN

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 7 21:10:00 2000; MasPar time 3.88 Seconds

Tubular output not generated. 122.160 Million cell updates/sec

Title: >US-08-981-824-1  
Description: (1-20) from US08981824.pep  
Perfect Score: 146  
Sequence: 1 DVNYAFHLATDLLPACDGER 20

Scoring table: PAM 150  
Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 08.  
Listing first 45 summaries

Database: f:geneseq35  
i:geneseqp

Statistics: Mean=20.820; Variance 63.757; scale 0.327

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	146	100.0	20	1	W01793 Human 65 kD glutamine	4.60e-09
2	146	100.0	20	1	W18842 65 kD Glutamic acid de	4.60e-09
3	146	100.0	503	1	R23645 Human GAD65 gene produ	4.60e-09
4	146	100.0	540	1	R59520 GAD65 1-45 N-terminal-	4.60e-09
5	146	100.0	544	1	R59524 GAD65 545-585 C-termin	4.60e-09
6	146	100.0	534	1	R59518 GAD65 1-31 deleted, C4	4.60e-09
7	146	100.0	584	1	W86017 Human GAD65 protein se	4.60e-09
8	146	100.0	584	1	W34519 Human GAD65 protein.	4.60e-09
9	146	100.0	585	1	W12402 65 kD human glutamic a	4.60e-09
10	146	100.0	585	1	W14915 Modified glutamic acid	4.60e-09
11	146	100.0	585	1	R28756 Human pancreatic islet	4.60e-09
12	146	100.0	585	1	R59516 Human GAD65.	4.60e-09
13	146	100.0	585	1	R79105 Human glutamic acid de	4.60e-09
14	146	100.0	585	1	W14916 Modified glutamic acid	4.60e-09
15	146	100.0	585	1	R71541 Human GAD.	4.60e-09
16	146	100.0	585	1	R29629 Human GAD 65.	4.60e-09
17	146	100.0	585	1	W35361 Human 65K-glutamic aci	4.60e-09
18	135	92.5	585	1	R23644 Rat GAD65 gene product	1.07e-07
19	135	92.5	585	1	R29628 Rat GAD 65.	1.07e-07
20	135	92.5	605	1	R71733 Rat glutamic acid deca	1.07e-07
21	129	88.4	584	1	W86018 Rat GAD65 protein sequ	5.88e-07
22	129	88.4	584	1	W34520 Rat GAD65 protein.	5.88e-07
23	128	87.7	540	1	R59521 GAD65 1-45 N-terminal-	7.80e-07

24	128	87.7	544	1	R59525 GAD65 545-585 C-termin	7.80e-07
25	128	87.7	554	1	R59519 GAD65 1-31 deleted, C4	7.80e-07
26	128	87.7	585	1	R59517 Rat GAD65.	7.80e-07
27	99	67.8	14	1	R75649 Peptide derived from h	2.38e-03
28	99	67.8	14	1	W18857 65 kD Glutamic acid de	2.38e-03
29	93	63.7	20	1	R72267 Glutamic acid decarbox	1.19e-02
30	85	58.2	20	1	R72266 Glutamic acid decarbox	9.85e-02
31	63	43.2	533	1	R37585 E.coli malate synthase	2.49e+01
32	61	41.8	593	1	R27220 Brain GAD #2.	4.01e+01
33	61	41.8	594	1	R27221 Full length brain GAD.	4.01e+01
34	61	41.8	594	1	R74716 Amino acid sequence of	4.01e+01
35	61	41.8	594	1	R74717 Amino acid sequence of	4.01e+01
36	61	41.8	594	1	R27222 Full length islet GAD.	4.01e+01
37	61	41.8	666	1	W31268 Mouse frizzled-3 prote	4.01e+01
38	58	39.7	190	1	R98922 Murine APLP1 (aa21-210	8.12e+01
39	58	39.7	273	1	W82006 Human adult brain secr	8.12e+01
40	58	39.7	343	1	R97222 Human G-protein couple	8.12e+01
41	58	39.7	424	1	R63441 Trichoderma harzianum	8.12e+01
42	58	39.7	653	1	R98903 Murine APLP1.	8.12e+01
43	58	39.7	663	1	R40923 Alcohol oxidase.	8.12e+01
44	57	39.0	848	1	R80551 Human Ah receptor prot	1.02e+02
45	57	39.0	2707	1	W27161 Mouse receptor ME2.	1.02e+02

ALIGNMENTS

RESULT 1

ID W01793 standard; peptide; 20 AA.  
AC W01793;  
DT 25-OCT-1997 (first entry)  
DE Human 65 kD glutamine decarboxylase peptide.  
KW Human; glutamine decarboxylase; GAD; diagnosis; predisposition;  
KW tumour; immunological; disease; autoimmune; diabetes; reagent;  
KW determination; T cell; subpopulation; medication; treatment;  
KW prevention; production; antigen; immunogen; tolerogen; isolation;  
KW reinjection; inactivation.  
OS Homo sapiens.  
PN DE19525784-A1.  
PD 16-JAN-1997. 025784.  
PF 14-JUL-1995; DE-025784.  
PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
PI Albert W. Boitard C. Endl J. Jung G. Schendel D;  
PI Stahl P. Van Endert P;  
DR WPI: 97-078452/08.  
PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of  
PT diabetes, etc.  
PS Claim 1; Page 12; 15pp; German.  
CC The present peptide is a fragment of the human 65 kD glutamine  
CC decarboxylase (GAD), which can be used to diagnose, or diagnose a  
CC predisposition to, a tumour or immunological disease, preferably an  
CC autoimmune disease, especially diabetes. It can also be used as a  
CC reagent to determine specific T cell subpopulations, in medicaments  
CC to treat or prevent immunological diseases, preferably autoimmune  
CC diseases, especially diabetes, to produce antigens, especially  
CC immunogens or tolerogens and to isolate specific T cell  
CC subpopulations, which can be used to produce antigens or for  
CC reinjection, optionally after inactivation.  
SQ Sequence 20 AA;

Query Match 100.0%; Score 146; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 4.60e-09; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Db 1 DVNYAFHLATDLLPACDGER 20

Qy 1 DVNYAFHLATDLLPACDGER 20

RESULT 2

ID W18842 standard; peptide; 20 AA.

AC W18842;

DT 05-JAN-1998 (first entry)

DE 65 kD Glutamic acid decarboxylase peptide fragment I.  
 KW GAD; 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;  
 KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;  
 KW predisposition; autoimmune; tumour; rheumatoid arthritis;  
 KW multiple sclerosis.  
 OS Synthetic.  
 PN DE19526561-A1  
 PD 23-JAN-1997  
 PF 20-JUL-1995; 026561.  
 PR 20-JUL-1995; DE-026561.  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 PI Donie F, Endl J, Ganz M, Jung G, Kientsch-engel R;  
 PI Pozzilli P, Stahl P;  
 DR WPI: 97-088254/09.  
 PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -  
 PT involving intradermal admin. of auto-reactive substances  
 PS Claim 11; Page 9; 12pp; German.  
 CC W18842-70 are peptide fragments of the 65 kD human glutamic acid  
 CC decarboxylase (GAD). The fragments are autoreactive substances used for  
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is  
 CC determined by using a claimed method for diagnosis of cell-mediated  
 CC diseases or a predisposition to cell-mediated diseases, which is effected  
 CC by administering an autoreactive substance intradermally and establishing  
 CC the diagnosis on the basis of the occurrence or lack of a positive  
 CC reaction at the site of administration. The method is used for diagnosis  
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases  
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 146; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DVNYAFLHATDLLPACDGER 20  
 I|||||I|||||I|||||I  
 QY 1 DVNYAFLHATDLLPACDGER 20

RESULT 3  
 ID R23645 standard; Protein; 503 AA.  
 AC R23645;  
 DT 02-NOV-1992 (first entry)  
 DE Human GAD65 gene product  
 DE Glutamic acid decarboxylase; IDDM; stiff man syndrome;  
 KW autoantibodies.  
 OS Homo sapiens.  
 PN WO9205446-A.  
 PD 02-APR-1992.  
 PF 23-SEP-1991; 006872.  
 PR 21-SEP-1990; US-586536.  
 PA (REGC ) UNIV CALIFORNIA.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Erlanger MG, Kaufman DL, Tobin AJ;  
 DR WPI: 92-150489/18.  
 DR N-PSDB: Q24184.

PT Novel cDNA encoding GAD65 polypeptide - used to produce GAD65 for  
 PT therapeutic and diagnostic application in insulin-dependent  
 PT diabetes mellitus patients  
 PS Disclosure: Fig 3; 53pp; English.  
 CC The sequence given is a glutamic acid decarboxylase (GAD65). GAD65  
 CC can be used for the diagnosis and therapy of patients with autoimmune  
 CC diseases, esp. insulin-dependent diabetes mellitus (IDDM) and "stiff  
 CC man" syndrome. It is possible to use either the entire GAD65 protein  
 CC or polypeptide fragments of it for the immunological detection of  
 CC autoantibodies to GAD65 which are indicative of IDDM and other auto-  
 CC immune diseases. The production of this sequence by recombinant DNA  
 CC technology allows large scale production of eukaryotic GAD65 in its  
 CC native form without the need for separation from other proteinaceous  
 CC prods.  
 SQ Sequence 503 AA;

Query Match 100.0%; Score 146; DB 1; Length 503;

Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFLHATDLLPACDGER 105  
 I|||||I|||||I|||||I  
 QY 1 DVNYAFLHATDLLPACDGER 20

RESULT 4  
 ID R59520 standard; protein; 540 AA.  
 AC R59520;  
 DT 03-NOV-1994 (first entry)  
 DE GAD65 1-45 N-terminal-deleted mutant.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody; mutagenesis.  
 OS Homo sapiens.  
 PN WO9412529-A.  
 PD 03-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure; Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 540 AA;

Query Match 100.0%; Score 146; DB 1; Length 540;

Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 41 DVNYAFLHATDLLPACDGER 60  
 I|||||I|||||I|||||I  
 QY 1 DVNYAFLHATDLLPACDGER 20

RESULT 5  
 ID R59524 standard; protein; 544 AA.  
 AC R59524;  
 DT 09-NOV-1994 (first entry)  
 DE GAD65 545-585 C-terminal-deleted mutant.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody; mutagenesis.  
 OS Homo sapiens.  
 PN WO9412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure; Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. The C-terminally deleted mutants given in R59524-25  
 CC are able to recognize IDDM autoantibodies having the specificity  
 CC of MICA4/MICA6, but not those having the specificity of MICA1/MICA3  
 CC or MICA2. These mutants also have some N-terminal modifications  
 CC to improve solubility.  
 SQ Sequence 544 AA;

Query Match 100.0%; Score 146; DB 1; Length 544;  
Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFHATDLPACDGER 105  
QY 1 DVNYAFHATDLPACDGER 20

RESULT 6  
ID R59518 standard; protein; 554 AA.  
AC R59518;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-31 deleted, C45A mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI; 94-200193/24.  
DT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure; Fig. 1; 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 554 AA;

Query Match 100.0%; Score 146; DB 1; Length 554;  
Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 DVNYAFHATDLPACDGER 74  
QY 1 DVNYAFHATDLPACDGER 20

RESULT 7  
ID W86017 standard; protein; 584 AA.  
AC W86017;  
DT 22-FEB-1999 (first entry)  
DE Human GAD65 protein sequence.  
KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
KW Insulin-dependent diabetes mellitus; stiff man syndrome.  
OS Homo sapiens.  
PN US5849506-A.  
PD 15-DEC-1998.  
PF 25-MAY-1995; 450755.  
PR 02-DEC-1993; US-161290.  
PR 03-DEC-1992; US-984935.  
PR 25-MAY-1995; US-450755.  
PA (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI; 99-069720/06.  
DT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
PT diabetes and stiff man syndrome  
PS Examples; Fig 1; 31pp; English.  
CC This represents a human GAD65 protein sequence. The invention provides  
CC soluble fragments of GAD65 that are specifically reactive with at least  
CC one class of GAD65 autoantibody. The fragments are substantially free of  
CC N-terminal amino acids that would otherwise limit solubility. Different  
CC fragments contain different epitopes for different classes of GAD65  
CC autoantibodies. These fragments are used in the methods of the invention  
CC for detection of GAD65 autoantibodies. The methods are used for  
CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and

CC stiff man syndrome.  
SQ Sequence 584 AA;

Query Match 100.0%; Score 146; DB 1; Length 584;  
Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFHATDLPACDGER 105  
QY 1 DVNYAFHATDLPACDGER 20

RESULT 8  
ID W34519 standard; protein; 584 AA.  
AC W34519;  
DT 24-MAR-1998 (first entry)  
DE Human GAD65 protein.  
KW GAD65; glutamic acid decarboxylase protein; human; soluble fragment;  
KW autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
KW stiff man syndrome; therapy.  
OS Homo sapiens.  
PN US5891448-A.  
PD 23-NOV-1997.  
PF 02-DEC-1993; 161290.  
PR 02-DEC-1993; US-161290.  
PR 03-DEC-1992; US-984935.  
PA (BAEK/) BAEKESKOV S.  
PA (KIMJ/) KIM J.  
PA (NAMC/) NAMCHUK M.  
PA (RICH/) RICHTER W.  
PA (SHIY/) SHI Y.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI; 98-017711/02.  
DT Soluble fragments of glutamic acid decarboxylase GAD65 - used to  
PT distinguish between insulin-dependent diabetes mellitus and  
PT stiff-man syndrome  
PS Disclosure; column 27-30; 30pp; English.  
CC This sequence represents the human glutamic acid decarboxylase protein  
CC GAD65. The invention relates to soluble fragments of a GAD65 protein that  
CC are specifically reactive with a GAD65 autoantibody (AAB), where the  
CC fragment is at least 99% pure and the AAB binds to a conformational  
CC epitope of the fragment. The soluble GAD65 fragments can be used to  
CC distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff  
CC man syndrome. They can also be used for diagnosis and treatment of IDDM  
CC and stiff man syndrome. The fragments can distinguish different temporal  
CC stages in the progression of IDDM.  
SQ Sequence 584 AA;

Query Match 100.0%; Score 146; DB 1; Length 584;  
Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFHATDLPACDGER 105  
QY 1 DVNYAFHATDLPACDGER 20

RESULT 9  
ID W12402 standard; protein; 585 AA.  
AC W12402;  
DT 08-OCT-1997 (first entry)  
DE 65 KD human glutamic acid decarboxylase isoform.  
KW 65 KD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;  
KW neuron; central nervous system; type I diabetes; autoimmune response;  
KW T cell; therapy.  
OS Homo sapiens.  
PN WO9700891-A1.  
PD 09-JAN-1997.  
PF 24-JUN-1996; U10790.  
PR 23-JUN-1995; US-494624.  
PR (KENN-) KENNEDY INST RHEUMATOLOGY.  
PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.

PI Conlon PJ, Gaur A, Leslie RDG, Ling N, Londei M;  
 DR WPI: 97-087322/08.  
 DR N-PSDB; T61097.  
 PT New human glutamic acid decarboxylase peptide(s) - used for  
 PT treatment, diagnosis and determining predisposition to diabetes and  
 PT for ameliorating auto-immune responses.  
 PS Disclosure: Fig 1: 28pp; English.  
 CC This sequence represents the 65 kD isoform of human glutamic acid  
 CC decarboxylase (GAD65). GAD is an enzyme expressed in the beta cells of  
 CC the pancreas, and in neurons of the central nervous system. There are two  
 CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of  
 CC GAD65 have been identified in Type I diabetic patients. Fragments of  
 CC GAD65, and analogues of the fragments, are used in the methods of the  
 CC invention. The methods are for detecting or treating diabetes or a  
 CC predisposition to diabetes. The peptides can also be used for  
 CC ameliorating an autoimmune response in a patient. Alteration of the  
 CC native peptides with selective changes of crucial residues can induce  
 CC unresponsiveness or change the responsiveness of antigen-specific  
 CC autoreactive T cells. The peptide analogues compete for binding to MHC  
 CC and do not cause proliferation of the corresponding native  
 CC peptide-specific T cells.  
 SO Sequence 585 AA;  
  
 Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Db 86 DVNYAFHLHATDLLPACDGER 105  
 QY 1 DVNYAFHLHATDLLPACDGER 20  
 |||||  
 RESULT 10  
 ID W14915 standard; Protein; 585 AA.  
 AC W14915;  
 DE 10-JUL-1997 (first entry)  
 DT Modified glutamic acid decarboxylase (K396F).  
 KW Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;  
 KW insulin-dependent diabetes mellitus; vaccine;  
 KW enzyme engineering; protein engineering.  
 OS Synthetic.  
 PN WO9712034-A1.  
 PD 03-APR-1997.  
 PF 27-SEP-1996; SE1210.  
 PR 29-SEP-1995; SE-003379.  
 PA (SYNE-) SYNETICS BIOTECHNOLOGY AB.  
 PI Essen-Moeller A, Falorni A, Lernmark A, Robertson J;  
 DR WPI: 97-212895/19.  
 DR N-PSDB; T64560.  
 PT Modified glutamic acid decarboxylase for autoimmune disease  
 PT treatment - has immunoreactivity of unmodified GAD65 but decreased  
 PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus  
 PT treatment  
 PS Claim 3: Page 13-15; 24pp; English.  
 CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the  
 CC native lysine residue at amino acid position 396 replaced by  
 CC arginine. It is obtd. by site-directed mutagenesis (see also  
 CC T64561) of native human GAD65 cDNA and expression of the mutant DNA  
 CC (T64560) in transformed host cells. Lys-396 is critical for enzyme  
 CC activity. By replacing it with an amino acid incapable of Schiff  
 CC base formation, immunoreactivity is maintained but enzyme activity  
 CC is reduced or lost, so minimising the risk of toxicity. The  
 CC modified GAD can be used to treat and/or prevent autoimmune  
 CC disorders such as insulin-dependent diabetes mellitus (IDDM) and  
 CC other diseases, e.g. neurological diseases, esp. in individuals  
 CC having a genetic predisposition for IDDM or with an increased  
 CC antibody titre against GAD.  
 SO Sequence 585 AA;  
  
 Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVNYAFHLHATDLLPACDGER 105  
 QY 1 DVNYAFHLHATDLLPACDGER 20  
 |||||  
 RESULT 11  
 ID R28756 standard; Protein; 585 AA.  
 AC R28756;  
 DT 20-APR-1993 (first entry)  
 DE Human pancreatic islet cell glutamic acid decarboxylase.  
 KW GAD; insulin dependent diabetes mellitus; IDDM; autoantibody detection.  
 OS Homo sapiens.  
 PN WO9220811-A.  
 PD 26-NOV-1992.  
 PF 14-MAY-1992; U04079.  
 PR 15-MAY-1991; US-702162.  
 PA (UNIW ) UNIV WASHINGTON.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Foster DC, Grubin CE, Hagopian W, Karlisen AE, Lernmark A, Ohara PJ;  
 DR WPI: 92-415789/50.  
 DR N-PSDB; Q31783.  
 PT Polynucleotide encoding human islet glutamic acid decarboxylase -  
 PT used to test for auto-antibodies against itself to diagnose  
 PT insulin dependent diabetes mellitus  
 PS Disclosure; Fig 2: 45pp; English.  
 CC The sequence is that of human pancreatic islet glutamic acid  
 CC decarboxylase (GAD) which is used to test biological samples for  
 CC the presence of autoantibodies to human GAD. It can also be used  
 CC to remove antibodies against GAD from plasma in order to treat an  
 CC autoimmune response to GAD, e.g. in insulin-dependent diabetes  
 CC (IDDM), and may also be used to induce immunological tolerance to GAD  
 CC by giving GAD that specifically binds the GAD receptor on immature T  
 CC or B cells.  
 SO Sequence 585 AA;  
  
 Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Db 86 DVNYAFHLHATDLLPACDGER 105  
 QY 1 DVNYAFHLHATDLLPACDGER 20  
 |||||  
 RESULT 12  
 ID R59516 standard; protein; 585 AA.  
 AC R59516;  
 DT 09-NOV-1994 (first entry)  
 DE Human GAD65.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody.  
 OS Homo sapiens.  
 PN WO9412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure; Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SO Sequence 585 AA;  
  
 Query Match 100.0%; Score 146; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 4.60e-09;



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Matches      20; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Db      86 DVNYAFELHATDLLPACDGER 105
      |||||||
QY      1 DVNYAFELHATDLLPACDGER 20

RESULT 13
ID R79105 standard; Protein: 585 AA.
AC R79105;
DT 13-NOV-1995 (first entry)
DE Human glutamic acid decarboxylase (GAD65).
KW Rat glutamic acid decarboxylase; GAD65; autoimmune disorders;
OS insulin-dependent diabetes mellitus; stiff man disease.
PN Homo sapiens.
PN WO9507992-A.
PD 23-MAR-1995.
PF 24-AUG-1994; U09478.
PR 17-SEP-1993; US-123859.
PA (REGC ) UNIV CALIFORNIA.
PI Clare-Selzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
DR WPI: 95-131360/17.
DR N-PSDB; Q86482.
PT New polypeptide fragments of glutamic acid decarboxylase - for
PT diagnosis and treatment of autoimmune disease, esp. insulin
PT dependent diabetes, also related nucleic acid, vectors,
PT antibodies, hybridoma(s) etc.
PS Example 1; Fig 3; 100pp; English.
CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
CC acid decarboxylase (GAD65) respectively, from which the GAD65
CC fragments described in R72261-R72298 were derived. These fragments
CC can be used to detect autoantibodies against GAD, e.g. to diagnose
CC and treat GAD-related autoimmune disorders, such as insulin
CC dependent diabetes mellitus or stiff man disease.
SQ Sequence 585 AA;

Query Match      100.0%; Score 146; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.60e-09;
Matches      20; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Db      86 DVNYAFELHATDLLPACDGER 105
      |||||||
QY      1 DVNYAFELHATDLLPACDGER 20

RESULT 14
ID W14916 standard; Protein: 585 AA.
AC W14916;
DT 10-JUL-1997 (first entry)
DE Modified glutamic acid decarboxylase.
KW Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;
KW insulin-dependent diabetes mellitus; vaccine;
KW enzyme engineering; protein engineering.
OS Synthetic.
FH Key
FT misc_difference 396
FT /label= Ile, Arg, Gln, His, Gly
PN WO9712034-A1.
PD 03-APR-1997.
PF 27-SEP-1996; SE1210.
PR 29-SEP-1995; SE-003379.
PA (SYNE-) SYNETICS BIOTECHNOLOGY AB.
PI Essen-Moeller A, Falorni A, Lernmark A, Robertsson J;
DR WPI: 97-212895/19.
PT Modified glutamic acid decarboxylase for autoimmune disease
PT treatment - has immunoreactivity of unmodified GAD65 but decreased
PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus
PT treatment
PS Claim 1; Page 16-18; 24pp; English.
CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the
CC native Lys residue at amino acid position 396 replaced by Ile, Gln,
CC His, Gly or esp. Arg (see also W14915). It is obtd by site-
CC directed mutagenesis of native human GAD65 cDNA and expression of

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CC the mutant DNA in transformed host cells. Lys-396 is critical for
CC enzyme activity. By replacing it with an amino acid incapable of
CC Schiff base formation, immunoreactivity is maintained but enzyme
CC activity is reduced or lost, so minimising the risk of toxicity.
CC The modified GAD can be used to treat and/or prevent autoimmune
CC disorders such as insulin-dependent diabetes mellitus (IDDM) and
CC other diseases, e.g. neurological diseases, esp. in individuals
CC having a genetic predisposition for IDDM or with an increased
CC antibody titre against GAD.
SQ Sequence 585 AA;

Query Match      100.0%; Score 146; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.60e-09;
Matches      20; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Db      86 DVNYAFELHATDLLPACDGER 105
      |||||||
QY      1 DVNYAFELHATDLLPACDGER 20

RESULT 15
ID R71641 standard; Protein: 585 AA.
AC R71641;
DT 21-SEP-1995 (first entry)
DE Human GAD.
KW GAD; glutamic-acid-decarboxylase; glutamate-decarboxylase;
KW non-insulin-dependent diabetes; NIDDM; diagnosis; autoantibody;
KW pancreas; islet.
OS Homo sapiens.
FH Key
FT binding_site
FT /label= Pyridoxal-5'-phosphate_binding_site
FT WO9507464-A.
PN 16-MAR-1995.
PF 02-SEP-1994; U09937.
PR 07-SEP-1993; US-117907.
PA (UNIW ) UNIV WASHINGTON.
PI Hagopian W, Karlisen AE, Landin-Olsson M, Lernmark A;
DR WPI: 95-123512/16.
DR N-PSDB; Q86046.
PT Predicting the clinical course of diabetes in patients with
PT non-insulin dependent diabetes mellitus - by detecting the
PT presence of auto-antibodies to human islet cell glutamic acid
PT decarboxylase.
PS Claim 8; Page 40-44; 62pp; English.
CC A human islet cDNA library was screened for colonies containing
CC GAD cDNA using probes (given in Q86047-49) based on conserved
CC internal and N- and C-terminal regions of cat, rat and mouse brain
CC GAD. Full-length clones were obtained by PCR-RACE. The entire
CC sequence of the human islet GAD cDNA is given in Q86046 and the
CC encoded protein in R71641. GAD was used to screen sera for the
CC presence of GAD autoantibodies.
SQ Sequence 585 AA;

Query Match      100.0%; Score 146; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 4.60e-09;
Matches      20; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Db      86 DVNYAFELHATDLLPACDGER 105
      |||||||
QY      1 DVNYAFELHATDLLPACDGER 20

Search completed: Tue Mar 7 21:10:07 2000
Job time : 7 secs.

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REFERENCE #A1935
#authors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.;
          Kautman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,
          A.J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
#cross-references GAD, are each encoded by a single gene.
#accession M1935
#molecule_type mRNA
#residues 1-585 #label BU1
#cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934
#experimental_source brain
#note
REFERENCE #A1292
#authors Karlisen, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
          Distèche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.;
          Grant, F.J.; Foster, D.; Lernermark, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
#title Cloning and primary structure of a human islet isoform of
#cross-references glutamic acid decarboxylase from chromosome 10.
#accession A1292
#molecule_type mRNA
#residues 1-585 #label KAR
#cross-references GB:M74826; NID:g182931; PIDN:AAA58491.1; PID:g182932
#experimental_source pancreatic islet
REFERENCE #S30058
#authors Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel,
          B.; Northemann, W.
#journal Eur. J. Biochem. (1993) 212:597-603
#title Characterization of a linear epitope within the human
#cross-references pancreatic 64-kDa glutamic acid decarboxylase and its
#cross-references autoimmune recognition by sera from insulin-dependent
#cross-references diabetes mellitus patients.
#accession S30058
#molecule_type mRNA
#residues 6-585 #label MAU
#cross-references EMBL:X69936
#experimental_source pancreatic islet
REFERENCE #A54778
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2)
#cross-references encoding two human glutamate decarboxylases (GAD-67 and
#cross-references GAD-65) suggests that they derive from a common ancestral
#cross-references GAD.
#cross-references M1935
#contents annotation; intron-exon boundaries
#comment This enzyme (GAD) catalyzes the formation of an inhibitory
#cross-references neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
#cross-references it has several isoforms, each encoded by a separate gene. GAD has
#cross-references also been implicated as an autoantigen in autoimmune disease
#cross-references stiff-man syndrome and insulin-dependent diabetes mellitus.
GENETICS #GDB:GAD2
#gene #cross-references GDB:128595; OMIM:138275
#map_position 10p11.23-10p11.23
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
          phosphate
FEATURE 396 #binding_site pyridoxal phosphate (Lys) (covalent)
          #status predicted
SUMMARY #length 585 #molecular-weight 65411 #checksum 4799
Query Match 100.0%; Score 146; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1,56e-19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 86 DYNVAFLLHATDLPACDGER 105
|||||

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QY 1 DYNVAFLLHATDLPACDGER 20
RESULT 3
ENTRY JC4064 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 65k chain - pig
#formal_name Sus scrofa domestica #common_name domestic pig
ORGANISM 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
DATE 22-Jun-1999
ACCESSIONS JC4064
REFERENCE JC4064
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
#journal Gene (1995) 152:257-260
#title Sequences of two porcine glutamic acid decarboxylases (65- and
#cross-references 67-kDa GAD).
#accession JC4064
#molecule_type mRNA
#residues 1-585 #label SUZ
#cross-references DDBJ:D1848; NID:g790964; PIDN:BA06635.1;
#cross-references PID:di007207; PID:g790965
#experimental_source brain
#comment This enzyme catalyzes the conversion of glutamic acid into
#cross-references gamma-amino butyric acid.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
FEATURE 393-396 #domain DOPA decarboxylase binding #status predicted
          #label BIN
SUMMARY #length 585 #molecular-weight 65388 #checksum 5933
Query Match 99.3%; Score 145; DB 2; Length 585;
Best Local Similarity 95.0%; Pred. No. 2,81e-19;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 86 EYNYAFLLHATDLPACDGER 105
|||||
QY 1 DYNVAFLLHATDLPACDGER 20
RESULT 4
ENTRY JH0423 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - rat
#formal_name Rattus norvegicus #common_name Norway rat
ORGANISM 31-Mar-1992 #sequence_revision 23-Mar-1995 #text_change
DATE 18-Jun-1999
ACCESSIONS JH0423; A60888
REFERENCE JH0423
#authors Erlander, M.G.; Tillakaratne, N.J.K.; Feldblum, S.; Patel,
          N.; Tobin, A.J.
#journal Neuron (1991) 7:91-100
#title Two genes encode distinct glutamate decarboxylases.
#cross-references M1935
#accession JH0423
#molecule_type mRNA
#residues 1-585 #label ERL
#cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226
#experimental_source brain
#note the authors translated the codon GAT for residue 86 as
#cross-references HIS, TCA for residue 198 as Ala, and CAG for residue
#cross-references 428 as Trp
REFERENCE A60888
#authors Chang, Y.C.; Gottlieb, D.I.
#journal J. Neurosci. (1988) 8:2123-2130
#title Characterization of the proteins purified with monoclonal
#cross-references antibodies to glutamic acid decarboxylase.
#accession A60888
#molecule_type preliminary
#residues 'V',191-194, 'X',196-203, 'XX',206-219, 'X',225-234, 'X',
#cross-references 236-247, 'X',249-266, 'X',524-537,539-543, 'V',547-549,

```

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid: it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase

KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 396 #binding-site pyridoxal phosphate (Lys) (covalent) #status predicted

SUMMARY #length 585 #molecular-weight 65402 #checksum 7756

Query Match 92.5%; Score 135; DB 1; Length 585; Best Local Similarity 90.0%; Pred. No. 9,76e-17; Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 86 DVMYALHATDLPACDGER 105  
1 DVMYALHATDLPACDGER 20

RESULT 5 #type complete

ENTRY B36182 #protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type

TITLE PTP69D precursor - fruit fly (*Drosophila melanogaster*)

ORGANISM #formal\_name *Drosophila melanogaster*

DATE 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999

ACCESSIONS B36182

REFERENCE A36182

KEYWORDS Streuli, M.; Krueger, N.X.; Tsai, A.Y.M.; Salco, H. Proc. Natl. Acad. Sci. U.S.A. (1989) 86:8698-8702

#journal A family of receptor-linked protein tyrosine phosphatases in humans and *Drosophila*.

#cross-references MIM:90046860

#accession B36182

#status preliminary: not compared with conceptual translation

#molecule-type mRNA

#residues 1-1462 #label STR

GENETICS #cross-references GB:M27699; NID:g158188; PIDN:AAA28842.1; PID:g158189

#gene PTP69D

CLASSIFICATION #cross-references FlyBase:FBgn0014007

#superfamily protein-tyrosine-phosphatase, receptor type

PTP69D; fibronectin type III repeat homology; immunoglobulin homology; leukocyte common antigen cytosolic domain homology; protein-tyrosine-phosphatase homology; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyrosine-specific phosphatase

KEYWORDS

FEATURE 1-28

29-1462 #domain signal sequence #status predicted #label SIG\

29-806 #product protein-tyrosine-phosphatase, receptor type

38-114 #domain extracellular #status predicted #label EXT\

147-216 #domain immunoglobulin homology #label IM1\

807-823 #domain immunoglobulin homology #label IM2\

824-1462 #domain transmembrane #status predicted #label TMN\

917-1145 #domain intracellular #status predicted #label INT\

1213-1439 #domain protein-tyrosine-phosphatase homology #label PTP1\

45-112,154-214 #disulfide-bonds #status predicted

1097 #active-site Cys (phosphocysteine intermediate) #status predicted

1103 #binding-site substrate phosphate (Arg) #status predicted

1391 #active-site Cys (phosphocysteine intermediate) #status predicted

1397 #binding-site substrate phosphate (Arg) #status predicted

SUMMARY #length 1462 #molecular-weight 167410 #checksum 8905

Query Match 45.2%; Score 66; DB 1; Length 1462; Best Local Similarity 35.0%; Pred. No. 4,97e-01; Matches 7; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 888 DTDYGLREYEMLPNRFSDR 907  
1 DVMYALHATDLPACDGER 20

RESULT 6 #type complete

ENTRY B44509

TITLE aldose 1-epimerase (EC 5.1.3.3) - *Streptococcus thermophilus*

ORGANISM #formal\_name *Streptococcus thermophilus*

DATE 10-Sep-1999 #sequence-revision 10-Sep-1999 #text-change 10-Sep-1999

ACCESSIONS B44509

REFERENCE B44509

KEYWORDS Poolman, B.; Royer, T.J.; Mainzer, S.E.; Schmidt, B.F. J. Bacteriol. (1990) 172:4037-4047

#journal Carbohydrate utilization in *Streptococcus thermophilus*: characterization of the genes for aldose 1-epimerase (mutarotase) and UDPglucose 4-epimerase.

#cross-references MIM:90299833

#accession B44509

#status preliminary

#molecule-type DNA

#residues 1-348 #label POO

CLASSIFICATION #cross-references EMBL:M38175; NID:g153748; PID:g153750

KEYWORDS #superfamily aldose 1-epimerase

SUMMARY #length 348 #molecular-weight 39012 #checksum 5351

Query Match 43.8%; Score 64; DB 1; Length 348; Best Local Similarity 57.1%; Pred. No. 1.18e-00; Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Db 221 ENTYDRKTTDLP 234  
1 DVMYALHATDLP 14

RESULT 7 #type complete

ENTRY DMECL

TITLE L-serine dehydratase (EC 4.2.1.13) 1 - *Escherichia coli*

ALTERNATE\_NAMES L-serine deaminase 1

ORGANISM #formal\_name *Escherichia coli*

DATE 30-Jun-1991 #sequence-revision 21-Nov-1997 #text-change 18-Jun-1999

ACCESSIONS F64942; JY0036

REFERENCE F64942

KEYWORDS Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y. Science (1997) 277:1453-1462

#journal The complete genome sequence of *Escherichia coli* K-12.

#title #cross-references MIM:97426617

#accession F64942

#status preliminary: nucleic acid sequence not shown; translation not shown

#molecule-type DNA

#residues 1-454 #label BLAT

#cross-references GB:AE000275; GB:U00096; NID:g1788106; PIDN:AAC74884.1; PID:g1788116; UNKP:bl814

REFERENCE JY0036

KEYWORDS #experimental-source strain K-12, substratum M6165

#journal Su, H.; Lang, B.F.; Newman, E.B. J. Bacteriol. (1989) 171:5095-5102

#title L-serine degradation in *Escherichia coli* K-12: cloning and sequencing of the *sda* gene.

#cross-references MIM:89359152

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#accession . JY0036
##molecule_type DNA
##residues 7-219,'N':221-454 ##label SUH
##cross-references GB:M8695
##experimental_source strain K12
COMMENT This enzyme converts L-serine to pyruvate.
GENETICS
#gene sda
CLASSIFICATION #superfamily microbial_L-serine dehydratase
KEYWORDS carbon-oxygen lyase; gluconeogenesis; hydro-lyase; lyase;
pyridoxal phosphate; serine catabolism
SUMMARY #length 454 #molecular-weight 48906 #checksum 2174

Query Match 43.8%; Score 64; DB 1; Length 454;
Best Local Similarity 50.0%; Pred. No. 1.1e+00;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 167 VPYPKSAATELLAYCN 182
OY 2 VNVAFLHATDLPCACD 17

RESULT 8
ENTRY #type complete
TITLE nudel protein precursor - fruit fly (Drosophila melanogaster)
ORGANISM #formal_name Drosophila melanogaster
DATE 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change
16-Jul-1999
ACCESSIONS A57096
REFERENCE A57096
#authors Hong, C.C.; Hashimoto, C.
#journal Cell (1995) 82:785-794
#title An unusual mosaic protein with a protease domain, encoded by
the nudel gene, is involved in defining embryonic
dorsoventral polarity in Drosophila.
#cross-references NUID:95401268
#accession A57096
##status preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues 1-2616 ##label HON
#cross-references GB:U29153; NID:9984320; PID:9984321
GENETICS
#gene FlyBase:ncl
FEATURES
##cross-references FlyBase:FBgn0002926
CLASSIFICATION #superfamily LDL receptor ligand-binding repeat homology;
trypsin homology
KEYWORDS extracellular protein
FEATURE
891-929 #domain LDL receptor ligand-binding repeat homology
#label LDL1\
1145-1378 #domain trypsin homology #label TRY\
1396-1430 #domain LDL receptor ligand-binding repeat homology
#label LDL7\
1776-1811 #domain LDL receptor ligand-binding repeat homology
#label LDL2\
2310-2344 #domain LDL receptor ligand-binding repeat homology
#label LDL8\
2421-2457 #domain LDL receptor ligand-binding repeat homology
#label LDL3
SUMMARY #length 2616 #molecular-weight 292372 #checksum 9962

Query Match 43.8%; Score 64; DB 2; Length 2616;
Best Local Similarity 47.1%; Pred. No. 1.1e+00;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Db 2390 FTYIQAIDPSKICGKR 2406
OY 4 YAFIAHDLDLPACDGER 20

RESULT 9
ENTRY #type complete
TITLE Killer toxin KP4 precursor - Ustilago maydis virus P4

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ORGANISM      #formal name Ustilago maydis virus P4, Univ-P4
DATE          19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
              13-Sep-1998
ACCESSIONS    S40034; S14734
REFERENCE     Park, C.M.; Brenn, J.A.; Ganesa, C.; Flurkey, W.F.; Bozarth, R.F.; Koltin, Y.
#authors      MoJ. Microbiol. (1994) 11:155-164
#journal      Structure and heterologous expression of the Ustilago maydis
#title        viral toxin KP4.
#cross-references M01D:94195103
#accession    S40034
##molecule_type mRNA
##residues    1-127 ##label PAR
REFERENCE     #cross-references EMBL:L12226
S14734
#authors      Ganesa, C.; Flurkey, W.H.; Randhawa, Z.I.; Bozarth, R.F.
#journal      Arch. Biochem. Biophys. (1991) 286:195-200
#title        Ustilago maydis vitus P4 killer toxin: characterization,
              partial amino terminus sequence, and evidence for
              glycosylation.
#cross-references M01D:91378288
#accession    S14734
##molecule_type protein
##residues    23-52 ##label GAN
KEYWORDS       toxin
FEATURE        #domain signal sequence #status predicted #label SIG
               #product killer toxin KP4 #status experimental #label
               MAT
SUMMARY        #length 127 #molecular-weight 13489 #checksum 9326
               MAP
Query Match    43.2%; Score 63; DB 2; Length 127;
Best Local Similarity 50.0%; Pied. NO. 1,80e+00;
Matches        7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db            5 NWYSFLEAAMP 18
              :|::|||::||
OY            1 DVNYAFLEHATDLDP 14

RESULT        10
ENTRY         SYSCMA           #type complete
TITLE         malate synthase (EC 4.1.3.2) A - Escherichia coli
ORGANISM      #formal_name Escherichia coli
DATE          31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
              18-Jun-1999
ACCESSIONS    A33649; E65208; Q00592
REFERENCE     S05692
#authors      Byrne, C.
#submitter    submitted to the EMBL Data Library, July 1988
#accession    A33649
##molecule_type DNA
##residues    1-533 ##label BYR1
REFERENCE     A30378
#authors      Byrne, C.R.; Stokes, H.W.; Ward, K.A.
#journal      Nucleic Acids Res. (1988) 16:10924
#title        Nucleotide sequence of the aceB gene encoding malate synthase
              A in Escherichia coli.
#cross-references M01D:89083515
#accession    A30378
##molecule_type DNA
##residues    1-533 ##label BYR2
REFERENCE     A64720
#authors      Blatter, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
              Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
              Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
              Kirpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
              Y.
              Science (1997) 277:1453-1462
#journal      The complete genome sequence of Escherichia coli K-12.
#title        The complete genome sequence of Escherichia coli K-12.
#cross-references M01D:97426617
#accession    E65208

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#status      preliminary: nucleic acid sequence not shown;
#molecule_type DNA
#residues    1-533 #label BLAT
#cross-references GB:AE000474; GB:U00096; NID:91790440;
                PID:91790444; UMGCP:bd014
#experimental_source strain K-12, substrain MG1655
GENETICS
#map_position 91 min
CLASSIFICATION #superfamily malate synthase
KEYWORDS      carbon-carbon lyase: glyoxylate bypass: oxo-acid-lyase
SUMMARY       #length 533 #molecular-weight 60273 #checksum 1098

Query Match    43.2%; Score 63; DB 1; Length 533;
Best Local Similarity 66.7%; Pred. No. 1.80e+00;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 402 ADOLAPDGER 413
QY 9 ATDLPPACDGER 20

RESULT 11
ENTRY  A72009 #type complete
TITLE  fumarate hydratase Chlamydia pneumoniae (strain CWL029)
ORGANISM #formal_name Chlamydia pneumoniae
DATE 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change
22-Jun-1999
ACCESSIONS A72009
REFERENCE A72000
#authors Kaibman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.;
          Ollinger, L.; Grimwood, J.; Davis, R.W.; Stephens, R.S.
#journal Nature Genet. (1999) 21:385-389
#title Comparative genomes of Chlamydia pneumoniae and C.
          trachomatis.
#cross-references MIMD:99206606
#accession A72009
#status preliminary
#molecule_type DNA
#residues 1-460 #label ARN
#cross-references GB:AE001681; GB:AE001363; NID:94377330;
                PIDN:AD09150.1; PID:94377343
#experimental_source strain CWL029
GENETICS
#gene func
CLASSIFICATION #superfamily fumarate hydratase
SUMMARY #length 460 #molecular-weight 50441 #checksum 6630

Query Match    42.5%; Score 62; DB 2; Length 460;
Best Local Similarity 46.2%; Pred. No. 2.74e+00;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 362 IIFYNLOSVDLS 374
QY 2 VNYAFHATDLP 14

RESULT 12
ENTRY  S66947 #type complete
TITLE  hypothetical protein YOR064c - yeast (Saccharomyces
          cerevisiae)
ALTERNATE_NAMES #hypothetical protein O2815
ORANISM #formal_name Saccharomyces cerevisiae
DATE 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change
14-Nov-1997
ACCESSIONS S66947
REFERENCE S66929
#authors Bonn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang,
          D.V.; Valens, M.
#submission submitted to the Protein Sequence Database, July 1996
#accession S66947
#molecule_type DNA

#residues 1-219 #label BOH
#cross-references EMBL:Z74972; NID:91420208; PID:e251980; PID:91420209;
                MIPS:YOR064c
#experimental_source strain 5288C
GENETICS
#map_position 15R
SUMMARY #length 219 #molecular-weight 25350 #checksum 6074

Query Match    41.8%; Score 61; DB 2; Length 219;
Best Local Similarity 47.1%; Pred. No. 4.16e+00;
Matches 8; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Db 12 DIRSFSTIDHP-CE 27
QY 1 DVNYAFHATDLPACD 17

RESULT 13
ENTRY  I59173 #type complete
TITLE  glutamate decarboxylase - rat
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
22-Jun-1999
ACCESSIONS I59173
REFERENCE I59173
#authors Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.
          Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775
#journal Developmentally regulated expression of an exon containing a
          stop codon in the gene for glutamic acid decarboxylase.
#cross-references MIMD:91062362
#accession I59173
#status preliminary: translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-223 #label RES
#cross-references GB:M8350; NID:9204231; PIDN:AA41185.1; PID:9204232
CLASSIFICATION #superfamily human glutamate decarboxylase
SUMMARY #length 223 #molecular-weight 25069 #checksum 1388

Query Match    41.8%; Score 61; DB 2; Length 223;
Best Local Similarity 47.4%; Pred. No. 4.16e+00;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 91 ETDFSNLFADDLPAKNGE 109
QY 1 DVNYAFHATDLPACDGE 19

RESULT 14
ENTRY  S49897 #type complete
TITLE  hypothetical narbonin-like 2S protein (clone pVFNA4) - fava
          bean
ORGANISM #formal_name Vicia faba #common_name fava bean
DATE 05-Mar-1995 #sequence_revision 14-Jul-1995 #text_change
26-Aug-1999
ACCESSIONS S49897
REFERENCE S49848
#authors Nong, V.; Schlessier, B.; Muentz, K.
          submitted to the EMBL Data Library, November 1994
#description The narbonin gene from Vicia faba L.
#accession S49897
#status preliminary
#molecule_type mRNA
#residues 1-286 #label NON
#cross-references EMBL:Z46834; NID:9600103; PID:9600104
#experimental_source seed
CLASSIFICATION #superfamily alcohol sulfotransferase
KEYWORDS seed; storage protein
SUMMARY #length 286 #molecular-weight 32575 #checksum 1900

Query Match    41.8%; Score 61; DB 2; Length 286;
Best Local Similarity 31.3%; Pred. No. 4.16e+00;
Matches 5; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
```





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 (TW)

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MPsrch\_p protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Mar 7 21:02:37 2000; MasPar time 3.45 Seconds  
 Tabular output not generated. 173.144 Million cell updates/sec

Title: >US-08-981-824-1  
 Description: (1-20) from US08981824.dep  
 Perfect Score: 146  
 Sequence: 1 DVNVAFLNATDILPACDGER 20

Scoring table: PAM 150  
 Gap 15

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot38  
 1:swissprot

Statistics: Mean 29.144; Variance 36.336; scale 0.802

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	146	100.0	585	1 DCE2_HUMAN	GLUTAMATE DECARBOXYLASE	7.49e-22
2	146	100.0	585	1 DCE2_MOUSE	GLUTAMATE DECARBOXYLASE	7.49e-22
3	145	99.3	585	1 DCE2_PIG	GLUTAMATE DECARBOXYLASE	1.44e-21
4	135	92.5	585	1 DCE2_RAT	GLUTAMATE DECARBOXYLASE	8.98e-19
5	66	45.2	1462	1 PTP6_DROME	PROTEIN-TYROSINE PHOSPH	1.46e-01
6	64	43.8	454	1 GDM_STSTR	ALDOSE 1-EPIMERASE (EC	3.72e-01
7	64	43.8	454	1 SDHL_ECOLI	L-SERINE DEHYDRATASE 1	3.72e-01
8	64	43.8	2616	1 NDL_DROME	SERINE PROTEASE NUDEL	5.90e-01
9	63	43.2	127	1 KP4T_UNIV4	KP4 KILLER TOXIN PRECU	5.90e-01
10	63	43.2	396	1 YNAG_RHISN	HYPOTHETICAL 42.8 KD P	5.90e-01
11	63	43.2	533	1 MASY_ECOLI	MALATE SYNTHASE A (EC	5.90e-01
12	61	41.8	593	1 DCE1_MOUSE	GLUTAMATE DECARBOXYLASE	1.46e+00
13	61	41.8	593	1 DCE1_RAT	GLUTAMATE DECARBOXYLASE	1.46e+00
14	61	41.8	594	1 DCE1_PIG	GLUTAMATE DECARBOXYLASE	1.46e+00
15	61	41.8	594	1 DCE1_FELCA	GLUTAMATE DECARBOXYLASE	1.46e+00
16	61	41.8	594	1 DCE1_HUMAN	GLUTAMATE DECARBOXYLASE	1.46e+00
17	61	41.8	770	1 YRN9_CAEEL	HYPOTHETICAL 84.2 KD P	3.54e+00
18	59	40.4	133	1 YB88_YEAST	HYPOTHETICAL 15.5 KD P	3.54e+00
19	58	39.7	926	1 CLAA_LYCES	ATP-DEPENDENT CLP PROT	5.45e+00
20	58	39.7	361	1 TRMU_CHLNP	PROBABLE TUNA (5-METHY	5.45e+00
21	58	39.7	488	1 CAFA_ECOLI	CYTOPLASMIC AXIAL FILA	5.45e+00
22	58	39.7	650	1 APPI_HUMAN	AMYLOID-LIKE PROTEIN 1	5.45e+00
23	58	39.7	653	1 APPI_MOUSE	AMYLOID-LIKE PROTEIN 1	5.45e+00

24	58	39.7	663	1 ALOX_CANEO	ALCOHOL OXIDASE (EC 1.	5.45e+00
25	58	39.7	1394	1 CNG4_BOVIN	240 KD PROTEIN OF ROD	5.45e+00
26	58	39.7	1677	1 VIT1_ACITR	VITELLIOGENIN PRECURSOR	5.45e+00
27	57	39.0	288	1 YDO9_SCHPO	HYPOTHETICAL 31.5 KD P	8.36e+00
28	57	39.0	462	1 FUMH_BACSU	FUMARATE HYDRATASE, CL	8.36e+00
29	57	39.0	523	1 SRC_RSVPA	TYROSINE-PROTEIN KINAS	8.36e+00
30	57	39.0	526	1 SRC_RSVSR	TYROSINE-PROTEIN KINAS	8.36e+00
31	57	39.0	540	1 SRC_AVISR	TYROSINE-PROTEIN KINAS	8.36e+00
32	57	39.0	526	1 GRBE_HUMAN	GROWTH FACTOR RECEPTOR	8.36e+00
33	57	39.0	582	1 PME2_ARATH	PECTINSTERASE 2 (EC 3	8.36e+00
34	57	39.0	584	1 PME1_CITSI	PECTINSTERASE 1.1 PRE	8.36e+00
35	57	39.0	848	1 AHR_HUMAN	AH RECEPTOR (ARYL HYDR	8.36e+00
36	57	39.0	853	1 AHR_RAT	AH RECEPTOR (ARYL HYDR	8.36e+00
37	57	39.0	876	1 YNE9_YEAST	HYPOTHETICAL 98.9 KD P	8.36e+00
38	56	38.4	498	1 YAC3_SCHPO	HYPOTHETICAL 56.6 KD P	1.27e+01
39	56	38.4	637	1 MUTA_PROPR	METHYLMALONYL-COA MUTA	1.27e+01
40	56	38.4	646	1 PLAP_MOUSE	PHOSPHOLIPASE A-2-ACTI	1.27e+01
41	56	38.4	647	1 PLAP_RAT	PHOSPHOLIPASE A-2-ACTI	1.27e+01
42	56	38.4	909	1 CNG4_HUMAN	CYCLOC-NUCLEOTIDE-GATE	1.27e+01
43	56	38.4	4568	1 DYHC_CAEEL	DYNEIN HEAVY CHAIN, CY	1.27e+01
44	55	37.7	174	1 Y030_BPHP1	HYPOTHETICAL 20.8 KD P	1.93e+01
45	55	37.7	1274	1 BXF_CLOBO	BOTULINUM NEUROTOXIN T	1.93e+01

## ALIGNMENTS

RESULT ID	1	DCE2_HUMAN	STANDARD:	PRT:	585 AA.
AC	005329:				
DT	01-FEB-1996	(Rel. 33, Created)			
DT	01-FEB-1996	(Rel. 33, Last sequence update)			
DT	01-FEB-1996	(Rel. 33, Last annotation update)			
DE	GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)				
DE	(65 KD GLUTAMIC ACID DECARBOXYLASE).				
GN	GAD2 OR GAD65.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 92196068.				
RA	BU D.-F., ERLANDER M.G., HITZ B.C., TILLAKARATNE N.J., KAUFMAN D.L.,				
RA	WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;				
RT	"Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are				
RT	each encoded by a single gene."				
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 94375018.				
RA	BU D.-F., TOBIN A.J.;				
RT	"The exon-intron organization of the genes (GAD1 and GAD2) encoding				
RT	two human glutamate decarboxylases (GAD67 and GAD65) suggests that				
RT	they derive from a common ancestral GAD."				
RL	Genomics 21:222-228(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	TISSUE-PANCREATIC ISLETS;				
RA	KARLSN A.E., BARKEIER H., MATTHEWS S., GRANT F.J., FOSTER D.,				
RA	ADLER D.A., HARGOPIN W.A., GRUBIN C.E., DUBE S., DISTECHE C.M.,				
RA	LENNMARK A.;				
RT	"Cloning and primary structure of a human islet isoform of glutamic				
RT	acid decarboxylase from chromosome 10."				
RL	Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).				
RN	[4]				
RP	SEQUENCE OF 6-585 FROM N.A.				
RX	TISSUE-PANCREAS;				
RA	MEDLINE: 93185681.				
RA	MAUCH L., ABNEY C.C., BERG H., SCHERBAUM W.A., LLEDVOGEL B.,				
RA	NORTHMAN W.;				
RT	"Characterization of a linear epitope within the human pancreatic				
RT	64-kDa glutamic acid decarboxylase and its autoimmune recognition by				
RT	sera from insulin-dependent diabetes mellitus patients."				

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RL Eur. J. Biochem. 212:597-603(1993).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC DECARBOXYLASE.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: M81882; AAA62367.1; -.
CC EMBL: M74826; AAA58491.1; -.
CC EMBL: X69936; CAA49554.1; ALT_INIT.
CC EMBL: M70435; AAA52513.1; -.
CC PIR: A41292; A41292.
CC PIR: PQ0158; PQ0158.
CC MIM: 138275; -.
CC PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
CC PFAM: PF00282; Pyridoxal_dec; 1.
CC Neurotransmitter biosynthesis; Lyase; Decarboxylase;
CC Pyridoxal phosphate; Multigene family.
CC BINDING 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC SEQUENCE 585 AA; 65411 MW; 8AD2B62 CRC32;

Query Match 100.0%; Score 146; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.49e-22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 86 DVMYAFIHMATDLPACDGER 105
1 DVMYAFIHMATDLPACDGER 20
|||||
RESULT 2
ID DCE2_MOUSE STANDARD; PRT; 585 AA.
AC P48320; O35519;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD2 OR GAD65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NC [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-BRAIN;
RX MEDLINE: 94032481.
RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;
RT Cloning and sequence analysis of a murine cDNA encoding glutamate
RT decarboxylase (GAD65).
RL Biochim. Biophys. Acta 1216:157-160(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-BRAIN;
RX MEDLINE: 97115675.
RA ASADA H., KAWAMURA Y., NARUYAMA K., KUME H., DING R.G., JI F.Y.,
RA KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.;
RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase
RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but
RT are susceptible to seizures."
RL Biochem. Biophys. Res. Commun. 229:891-895(1996).
RN [3]
RP SEQUENCE OF 175-379 FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 94062679.

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RA FAULKNER-JONES B.E., CRAW D.S., KUN J., HARRISON L.C.;
RT "Localization and quantitation of expression of two glutamate
RT decarboxylase genes in pancreatic beta-cells and other peripheral
RT tissues of mouse and rat."
RL Endocrinology 133:2962-2972(1993).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- CORRECTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC DECARBOXYLASE.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: L16980; AAA93049.1; -.
CC EMBL: D42051; BAA22893.1; -.
CC EMBL: S67454; CAB32806.1; -.
CC MGD: MG1:95634; GAD2.
CC PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
CC PFAM: PF00282; Pyridoxal_dec; 1.
CC Neurotransmitter biosynthesis; Lyase; Decarboxylase;
CC Pyridoxal phosphate; Multigene family.
CC BINDING 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
CC CONFLICT 259 259 F -> S (IN REF. 2).
CC CONFLICT 319 319 I -> S (IN REF. 3).
CC CONFLICT 325 325 K -> E (IN REF. 2).
CC CONFLICT 499 499 P -> S (IN REF. 2).
CC SEQUENCE 585 AA; 65224 MW; 9B5C088 CRC32;

Query Match 100.0%; Score 146; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.49e-22;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 86 DVMYAFIHMATDLPACDGER 105
1 DVMYAFIHMATDLPACDGER 20
|||||
RESULT 3
ID DCE2_PIG STANDARD; PRT; 585 AA.
AC P48321;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD2 OR GAD65.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
NC [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 95137399.
RA SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
RT "Sequences of two porcine glutamic acid decarboxylases (65- and
RT 67-kDa GAD)."
RL Gene 152:257-260(1995).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- CORRECTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
-----
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SQ SEQUENCE 2616 AA: 292371 MW: 0FFD8412 CRC32:  
 Query Match 43.8%; Score 64; DB 1; Length 2616;  
 Best Local Similarity 47.1%; Pred. No. 3.72e-01;  
 Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
 DB 2390 EHYLOATDPSKICDKR 2406  
 QY 4 YAFHATDLPACDGER 20  
 RESULT 9  
 ID KP4T UMW4 STANDARD; PRT: 127 AA.  
 AC Q90121.  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE KP4 KILLER TOXIN PRECURSOR.  
 GN M2A.  
 OS Ustilago maydis p4 virus (UMV4) (UMV-P4).  
 OC Viruses; dsRNA viruses; Totiviridae; Totivirus.  
 RN (1)  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-79 AND 124-127.  
 RC STRAIN-7;  
 RX MEDLINE: 94195103.  
 RA PARK C.-M., BRUENN J.A., GANESA C., FLURKEY W.F., BOZARTH R.F.,  
 RA KOLIN Y.,  
 RA "Structure and heterologous expression of the Ustilago maydis viral  
 RT toxin KP4."  
 RL Mol. Microbiol. 11:155-164(1994).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-2B;  
 RA GU F., KHIWANI A.K., FLURKEY W.F., BOZARTH R.F., SMITH T.J., RANE S.,  
 RA Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.  
 RN (3)  
 RP CHARACTERIZATION, AND SEQUENCE OF 23-52.  
 RX MEDLINE: 91378288.  
 RA GANESA C., FLURKEY W.H., RANDHAWA Z.I., BOZARTH R.F.,  
 RA "Ustilago maydis virus p4 killer toxin: characterization, partial  
 RT amino terminus sequence, and evidence for glycosylation."  
 RL Arch. Biochem. Biophys. 286:195-200(1991).  
 RN (4)  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE: 96027102.  
 RA GU F., KHIWANI A., RANE S.G., FLURKEY W.H., BOZARTH R.F., SMITH T.J.,  
 RA "Structure and function of a virally encoded fungal toxin from  
 RT Ustilago maydis: a fungal and mammalian Ca2+ channel inhibitor."  
 RL Structure 3:805-814(1995).  
 CC -1- FUNCTION: THIS PROTEIN IS LETHAL TO SENSITIVE CELLS OF THE SAME OR  
 CC RELATED SPECIES. IT SPECIFICALLY INHIBITS VOLTAGE-GATED CALCIUM  
 CC CHANNELS. KILLS TARGET FUNGAL CELLS BY BLOCKING DIVALENT CATION  
 CC CHANNELS (VIA CALCIUM AND/OR MAGNESIUM CHANNELS).  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUPRACELLULAR LOCATION: SECRETED.  
 CC -1- MASS SPECTROMETRY: MW-11045; MW\_ERR-11; METHOD-MALDI;  
 CC RANGE-23-127.  
 CC -1- CAUTION: WAS SAID BY REF.3 TO BE GLYCOSYLATED, BUT THIS DOES NOT  
 CC SEEM TO BE THE CASE ACCORDING TO REF.1.  
 CC -----  
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 CC -----  
 CC EMBL: L12226; AAA89185.1; -  
 DR EMBL: U25179; AAA5041.1; -  
 DR PDB: 1KPT; 31-OCT-95.  
 KW Toxin; Signal; 3D-structure.  
 FT SIGNAL 1 22

FT CHAIN 23 127 KP4 KILLER TOXIN.  
 FT DISULFID 27 100  
 FT DISULFID 33 103  
 FT DISULFID 49 89  
 FT DISULFID 57 82  
 FT DISULFID 66 127  
 FT CONFLICT 56 56  
 FT CONFLICT 66 66  
 FT CONFLICT 67 66  
 FT CONFLICT 73 73  
 FT CONFLICT 74 74  
 FT CONFLICT 79 79  
 SQ SEQUENCE 127 AA: 13489 MW: AF63FB09 CRC32:  
 Query Match 43.2%; Score 63; DB 1; Length 127;  
 Best Local Similarity 50.0%; Pred. No. 5.90e-01;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 DB 5 NYVSEFLFAAMLP 18  
 QY 1 DVNYAFHATDLP 14  
 RESULT 10  
 ID YANG\_RHISN STANDARD; PRT: 396 AA.  
 AC P55579.  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE HYPOTHETICAL 42.8 KD PROTEIN YANG.  
 GN YANG.  
 OS Rhizobium sp. (strain NGR234).  
 OG Plasmid sym PNGR234a.  
 OC Bacteria; Proteobacteria; alpha subdivision: Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97305956.  
 RA FREIBERG C.A., FELLAY R., BAIRDOCH A., BROUGHTON W.J., ROSENTHAL A.,  
 RA PERRET X.,  
 RA "Molecular basis of symbiosis between Rhizobium and legumes."  
 RT Nature 387:394-401(1997).  
 RL Nature 387:394-401(1997).  
 CC -1- FUNCTION: PUTATIVE NUCLEOTIDE SUGAR EPIMERASE/DEHYDROGENASE.  
 CC -1- CORFACTOR: NAD OR NADP.  
 CC -1- SIMILARITY: SOME, TO UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2),  
 CC DUDP-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46) AND NAD(P)-DEPENDENT  
 CC CHOLESTEROL DEHYDROGENASES.  
 CC -----  
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 CC -----  
 CC EMBL: AE000087; AAB91786.1; -  
 DR PFBM; PF01370; Epimerase; 1.  
 KW Hypothetical protein; NAD; Plasmid.  
 SQ SEQUENCE 396 AA: 42842 MW: 5BCFDDDE CRC32:  
 Query Match 43.2%; Score 63; DB 1; Length 396;  
 Best Local Similarity 50.0%; Pred. No. 5.90e-01;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
 DB 243 KYQFVHSDLASAC 256  
 QY 3 NYAFHATDLPAC 16  
 RESULT 11  
 ID MASY\_ECOLI STANDARD; PRT: 533 AA.  
 AC P08997.

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RC TISSUE-BRAIN.
RA KATAROVA Z., SZABO G., MUGNAINI E., GREENSPAN R.:
RT "Molecular identification of the 62 kd form of glutamic acid
RL decarboxylase from the mouse."
RL Eur. J. Neurosci. 2:190-202(1990).
RN [2]
RP SEQUENCE OF 198-403 FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 94062679.
RA FULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.:
RT "Localization and quantitation of expression of two glutamate
RL decarboxylase genes in pancreatic beta-cells and other peripheral
RT tissues of mouse and rat."
RL Endocrinology 133:2962-2972(1993).
RC - FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC - CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC - COFACTOR: PYRIDOXAL PHOSPHATE.
CC - SUBUNIT: HOMODIMER (BY SIMILARITY).
CC - SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC
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CC
DR EMBL; Z49976; CAA90277.1; -.
DR EMBL; S67453; CAB32805.1; -.
DR MGd; MG1:95632; GAD1.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM; PF00282; Pyridoxal_dec; 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KM Pyridoxal phosphate; Multigene family.
FT BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT CONFLICT 234 234 E -> K (IN REF. 2).
FT CONFLICT 258 258 S -> T (IN REF. 1).
FT CONFLICT 360 360 D -> S (IN REF. 1).
SQ SEQUENCE 593 AA; 66584 MW; 63BC57AA CRC32;

Query Match 41.8%; Score 61; DB 1; Length 593;
Best Local Similarity 47.4%; Pred. NO. 1.46e+00;
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 91 ETDPSNLEFADLLPARKGE 109
QY I D V N Y A F L H A T D L L P A C D G E 19
I : : : : | | | | | : | : |

RESULT 13
ID DCELI_RAT STANDARD: PRT: 593 AA.
AC P18086;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DI 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91014354.
RA WYBORSKI R.J., BOND R.W., GOTTLIEB D.I.:
RT "Characterization of a cDNA coding for rat glutamic acid
RT decarboxylase."
RL Brain Res. Mol. Brain Res. 8:193-198(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90132703.

```

RA JULIEN J.F., SAWAMA P., MALLET J.;  
 RT "Rat brain glutamic acid decarboxylase sequence deduced from a cloned  
 RT cDNA.";  
 RL J. Neurochem. 54:703-705(1990).  
 RP [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE: 92020930.  
 RA MICHELSEN B.K., PETERSEN J.S., BOEL E., MOLDROP A., DYBERG T.,  
 RA MADSEN O.D.;  
 RT "Cloning, characterization, and autoimmune recognition of rat islet  
 RT glutamic acid decarboxylase in insulin-dependent diabetes mellitus";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 TYRDC).  
 CC -----  
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 CC -----  
 CC EMBL: M34445; AAC42037.1; -  
 CC EMBL: X57572; CAA40800.1; -  
 CC EMBL: X57573; CAA40801.1; -  
 CC EMBL: M76177; AAA4184.1; -  
 CC PIR: A41367; A41367.  
 CC PIR: A43756; A43756.  
 CC PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 CC PFAM: PF00282; Pyridoxal\_dec; 1.  
 CC KM Neurotransmitter biosynthesis: Lyase: Decarboxylase;  
 KW Pyridoxal phosphate: Multigene family;  
 FT BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 FT CONFICT 103 103 L -> V (IN REF. 2).  
 FT CONFICT 284 284 F -> S (IN REF. 2).  
 FT CONFICT 287 288 EH -> AD (IN REF. 2).  
 FT CONFICT 344 345 AG -> EA (IN REF. 2).  
 FT CONFICT 347 347 T -> I (IN REF. 2).  
 FT CONFICT 352 353 FD -> LE (IN REF. 2).  
 FT CONFICT 380 380 L -> R (IN REF. 2).  
 SQ SEQUENCE 593 AA: 66640 MW: 54086700 CRC32;  
 Query Match 41.8%; Score 61; DB 1; Length 593;  
 Best Local Similarity 47.4%; Pred. No. 1.46e+00;  
 Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 DB 91 EIDFSLFADLLPKNKE 109  
 YQ 1 DVNYAFLLHATDLPACDGE 19  
 RESULT 14  
 ID DCE1\_PIG STANDARD; PRT; 594 AA.  
 AC P48319;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 95137399.  
 RA SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;

RT "Sequences of two porcine glutamic acid decarboxylases (65- and  
 RT 67-kDa GAD)";  
 RL Gene 152:257-260(1995).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 TYRDC).  
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 CC -----  
 CC EMBL: D31849; BAA0636.1; -  
 CC PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 CC PFAM: PF00282; Pyridoxal\_dec; 1.  
 CC KM Neurotransmitter biosynthesis: Lyase: Decarboxylase;  
 KW Pyridoxal phosphate: Multigene family;  
 FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 SQ SEQUENCE 594 AA: 66894 MW: 69067900 CRC32;  
 Query Match 41.8%; Score 61; DB 1; Length 594;  
 Best Local Similarity 47.4%; Pred. No. 1.46e+00;  
 Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 DB 92 EIDFSLFADLLPKNKE 110  
 YQ 1 DVNYAFLLHATDLPACDGE 19  
 RESULT 15  
 ID DCE1\_FELCA STANDARD; PRT; 594 AA.  
 AC P14748;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-OCIPITIAL CORTEX;  
 RX MEDLINE: 87310623.  
 RA KOBAYASHI Y., KAUFMAN D.L., TOBIN A.J.;  
 RT "Glutamic acid decarboxylase cDNA: nucleotide sequence encoding an  
 RT enzymatically active fusion protein";  
 RL J. Neurosci. 7:2768-2772(1987).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 TYRDC).  
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 CC -----  
 CC EMBL: M18629; AAA51430.1; -  
 CC PIR: A45671; A45671.  
 CC PIR: A46758; A46758.



DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
DR PRAM: PF00282; Pyridoxal\_dec; 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family.  
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).  
SQ SEQUENCE 594 AA: 66824 MW: 3820778 CRC32;

Query Match 41.8%; Score 61; DB 1; Length 594;  
Best Local Similarity 47.4%; Pred. No. 1.46e+00;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Lb 92 ETDESNLFARDLLPAKNGE 110  
QY 1 DVNYAFLLHATDLPACDGE 19

Search completed: Tue Mar 7 21:02:42 2000  
Job time : 5 secs.

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(TM)

Msearch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:07:15 2000; MasPar time 6.72 Seconds  
206.310 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-981-824-1  
Description: (1-20) from US08981824.pep  
Perfect Score: 146  
Sequence: 1 DVNVAFLHATDLPACDGER 20

Scoring table: PAM 150  
Gap 15

Searched: 225878 seqs, 69334122 residues  
Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: sptrembl12  
1:sp:archaea 2:sp:bacteria 3:sp:fungi 4:sp:human  
5:sp:invertebrate 6:sp:mammal 7:sp:mhc 8:sp:organelle  
9:sp:phage 10:sp:plant 11:sp:rodent 12:sp:unclassified  
13:sp:vertebrate 14:sp:virus

Statistics: Mean 28.168; Variance 40.452; scale 0.696

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	143	97.9	126	6	P79258	GLUTAMIC ACID DECARBOX	6.35e+18
2	75	51.4	76	6	P79257	GLUTAMIC ACID DECARBOX	1.76e+02
3	68	46.6	374	14	Q9W157	97.3% IDENTICAL TO U7	3.92e-01
4	66	45.2	2262	5	Q9Y0E4	KLARISCHT PROTEIN.	9.23e-01
5	64	43.8	266	11	Q9WVG7	ODD-SKIPPED RELATED 1	2.13e+00
6	64	43.8	590	13	Q9Y1S8	GLUTAMATE DECARBOXYLAS	2.13e+00
7	63	43.2	277	5	Q20297	COSMID FAH10.	3.23e+00
8	63	43.2	329	5	Q46012	ZK228.7 PROTEIN.	3.23e+00
9	62	42.5	150	5	Q25107	LYSIN PRECURSOR.	4.86e+00
10	62	42.5	460	2	Q926P6	FUMARATE HYDRATASE.	7.28e+00
11	61	41.8	219	3	Q08465	CHROMOSOME XV READING	7.28e+00
12	61	41.8	223	11	Q63211	GLUTAMATE DECARBOXYLAS	7.28e+00
13	61	41.8	236	13	Q42504	HOMEBOX PROTEIN HOXC-	7.28e+00
14	61	41.8	254	2	Q47099	CS31A MINOR SUBUNIT PR	7.28e+00
15	61	41.8	286	10	Q4161	POTATIVE NARONIN-LIKE	7.28e+00
16	61	41.8	287	10	Q39486	POTATIVE NARONIN.	7.28e+00
17	61	41.8	321	5	P91354	SIMILARITY TO MYXOCOCC	7.28e+00
18	61	41.8	593	11	Q08685	67KD GLUTAMIC ACID DEC	7.28e+00
19	61	41.8	666	11	Q61086	FRIZZLED-3.	7.28e+00
20	60	41.1	111	14	Q65203	PEL11R.	1.09e+01

RESULT	ID	PRELIMINARY:	PRT:	126 AA.
1	P79258			
2	P79257			
3	Q9W157			
4	Q9Y0E4			
5	Q9WVG7			
6	Q9Y1S8			
7	Q20297			
8	Q46012			
9	Q25107			
10	Q926P6			
11	Q08465			
12	Q63211			
13	Q42504			
14	Q47099			
15	Q4161			
16	Q39486			
17	P91354			
18	Q08685			
19	Q61086			
20	Q65203			

## ALIGNMENTS

RESULT	ID	PRELIMINARY:	PRT:	126 AA.
1	P79258			
2	P79257			
3	Q9W157			
4	Q9Y0E4			
5	Q9WVG7			
6	Q9Y1S8			
7	Q20297			
8	Q46012			
9	Q25107			
10	Q926P6			
11	Q08465			
12	Q63211			
13	Q42504			
14	Q47099			
15	Q4161			
16	Q39486			
17	P91354			
18	Q08685			
19	Q61086			
20	Q65203			

OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;  
OC Macaca.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 96256692.  
RA MITSUSHIMA D., MARZBAN F., LUCHANSKY L.L., BURICH A.J., KEEN K.L.,  
RA DUNNING M., GOLOS T.G., TERASAWA E.;  
RT "Role of glutamic acid decarboxylase in the prepubertal inhibition of  
the luteinizing hormone releasing hormone release in female rhesus  
monkeys."  
RL J. Neurosci. 16:2563-2573(1996).  
DR EMBL; S82650; AAB46786.1; -  
FT NON TER 1  
SQ SEQUENCE 76 AA; 8143 MW; 1AB755D0 CRC32;  
  
Query Match 51.4%; Score 75; DB 6; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.76e-02;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 44 DILPACDGER 53  
Oy 11 DILPACDGER 20  
|||||  
  
RESULT 3  
ID 09WT57 PRELIMINARY; PRT; 374 AA.  
AC 09WT57;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE 97.3% IDENTICAL TO U7 GENE OF STRAIN U1102 OF HHV-6.  
GN U7.  
OS Human herpesvirus 6.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Betaherpesvirinae; Roseolovirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-HST;  
RA ISEGAWA Y., MUKAI T., NAKANO K., KAGAWA M., CHEN J., MORI Y.,  
RA SUNAGAWA T., SASIHARA J., ZOU P., KOSUGE H., YAMANISHI K.;  
RT "A comparison of the complete DNA sequences between human herpesvirus-  
RT 6 variant A and B."  
RL J. Virol. 0:0-0(1999).  
DR EMBL; AB021506; BAA78227.1; -  
SQ SEQUENCE 374 AA; 43081 MW; 3588A75C CRC32;  
  
Query Match 46.6%; Score 68; DB 14; Length 374;  
Best Local Similarity 33.3%; Pred. No. 3.92e-01;  
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
  
Db 23 LHFAPFQTEIVPCNDE 40  
Oy 2 VNYAFHATDLPACDGE 19  
:::|::|::|::|  
  
RESULT 4  
ID 09Y0E4 PRELIMINARY; PRT; 2262 AA.  
AC 09Y0E4;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE KLASICHT PROTEIN.  
GN KLAS.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MOSLEY-BISHOP K.L., LI Q., PATTERSON K., FISCHER J.A.;  
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157066; AAD43129.1; -  
SQ SEQUENCE 2262 AA; 245116 MW; E35504F7 CRC32;

Query Match 45.2%; Score 66; DB 5; Length 2262;  
Best Local Similarity 33.0%; Pred. No. 9.23e-01;  
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;  
  
Db 225 QTNVYIMDTNLDTCREAR 244  
Oy 1 DNYAFHATDLPACDGER 20  
:|::|::|:|  
  
RESULT 5  
ID 09WVG7 PRELIMINARY; PRT; 266 AA.  
AC 09WVG7;  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE ODD-SKIPPED RELATED 1 PROTEIN.  
GN OSR1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 9940011.  
RA SO P.L., DANIELIAN P.S.;  
RT "Cloning and expression analysis of a mouse gene related to Drosophila  
RT odd-skipped."  
RL Mech. Dev. 84:157-160(1999).  
DR EMBL; AF117814; AAD37115.1; -  
DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_3.  
KW Zinc-finger; Metal-binding; DNA-binding  
SQ SEQUENCE 266 AA; 29584 MW; 8A97D286 CRC32;  
  
Query Match 43.8%; Score 64; DB 11; Length 266;  
Best Local Similarity 38.9%; Pred. No. 2.13e+00;  
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
  
Db 20 NYSFLQAVNGIPTVPSDR 37  
Oy 3 NYAFHATDLPACDGER 20  
|||::|::|::|  
  
RESULT 6  
ID 09Y158 PRELIMINARY; PRT; 590 AA.  
AC 09Y158;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE 67.  
GN GAD67.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-WHITE LEGHORN;  
RA WABERG F.;  
RT "Characterization of glutamate decarboxylase in chicken."  
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
CC TYRDC).  
DR EMBL; AF030355; AAD01902.1; -  
DR PROSITE; PS00392; DDC\_GAD\_HDC\_YDC\_1.  
KW Lysase; Decarboxylase; Pyridoxal phosphate.  
SQ SEQUENCE 590 AA; 66710 MW; 80B66DF6 CRC32;  
  
Query Match 43.8%; Score 64; DB 13; Length 590;  
Best Local Similarity 47.4%; Pred. No. 2.13e+00;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
  
Db 88 ETDPSNLARDLPAKNKE 106  
:|::|::|::|::|::|

OY 1 DVNYAFHLATDLPACDGE 19

RESULT 7  
ID Q020297 PRELIMINARY: PRT: 277 AA.

AC Q020297  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)  
DE COSMID F41H10.  
GN F41H10.5.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE: 94150718.  
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
RA JONES M., KERSHAW J., KIRSHEN J., LAISTER N., LATREILLE P.,  
RA JONES M., KERSHAW J., KIRSHEN J., LAISTER N., LATREILLE P.,  
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,  
RA THERRER-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).

RL Nature 368:32-38(1994).

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA BLANCHARD M., BRADSHAW H.;  
RN Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA WATERSTON R.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U61954; AAB03172.1; -;  
SO SEQUENCE 277 AA; 32024 MW; EBB04CAD CRC32;

Query Match 43.2%; Score 63; DB 5; Length 277;  
Best Local Similarity 50.0%; Pred. No. 3.23e+00;  
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 162 EVNSFLHARTLPLC 177  
OY 1 DVNYAFHLATDLPAC 16

RESULT 8  
ID Q46012 PRELIMINARY: PRT: 329 AA.

AC Q46012  
DT 01-JUN-1998 (TREMblrel. 06, Created)  
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
DE ZK228.7 PROTEIN.  
GN ZK228.7.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC BASHAM V.;  
RN Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 94150718.  
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
RA JONES M., KERSHAW J., KIRSHEN J., LAISTER N., LATREILLE P.,  
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULLSTON J.,  
RA THERRER-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
DR EMBL: 282086; CAB04998.1; -;  
DR PFM: PF01604; 7tm\_5; 1.1.  
SO SEQUENCE 329 AA; 36804 MW; 5E81A635 CRC32;

Query Match 43.2%; Score 63; DB 5; Length 329;  
Best Local Similarity 52.6%; Pred. No. 3.23e+00;  
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Db 63 DVNSFLAPVLTLPDGC 81  
OY 1 DVNYAFHLATDLPACDG 18

RESULT 9  
ID Q25107 PRELIMINARY: PRT: 150 AA.

AC Q25107  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
DE LYSIN PRECURSOR.  
OS Halictus ovina.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;  
OC Halictidae; Halictis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-TESTIS;  
RA LEE Y.H., VACQUIER V.D.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: L26276; AAA21522.1; -;  
DR HSSP: P04552; ILYN.  
DR PFM: PF01303; Egg\_Lysin; 1.  
KW Signal.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 150 LYSIN.  
SO SEQUENCE 150 AA; 17691 MW; 546D9513 CRC32;

Query Match 42.5%; Score 62; DB 5; Length 150;  
Best Local Similarity 50.0%; Pred. No. 4.86e+00;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 117 EVNSFLVRLNLP 130  
OY 1 DVNYAFHLATDLP 14

RESULT 10  
ID Q926P6 PRELIMINARY: PRT: 460 AA.

AC Q926P6  
DT 01-MAY-1999 (TREMblrel. 10, Created)  
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)  
DE FUMARATE HYDRATASE.  
GN FUMC.  
OS Chlamydia pneumoniae.  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CWL029;  
RA KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L.,  
RA GRIMWOOD J., DAVIS R.W., STEPHENS R.S.;  
RT "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AE001681: AAD19150.1; -  
 DR HSSP: P05042: 1FUO;  
 DR PROSITE: PS00163: FUMARATE\_LYASES; 1;  
 SQ SEQUENCE 460 AA; 50441 MW; AA418380 CRC32;  
 Query Match 42.5%; Score 62; DB 2; Length 460;  
 Best Local Similarity 46.2%; Pred. No. 4.86e+00;  
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 362 IITNLSQVDDL 374  
 : : : : :  
 QY 2 DVNYAFLLHATDLPACD 14

RESULT 11  
 ID 008465 PRELIMINARY; PRT; 219 AA.  
 AC 008465: 000025;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE CHROMOSOME XV READING FRAME ORF YOR064C.  
 GN YOR29-15.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;  
 OC Saccharomycetaceae; Saccharomycetes.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA BOHN C., BOLOTIN-FUKUHARA M., DAIGNAN-FORNIER B., DANG D.V.,  
 RA VALENS M.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPs;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97279235.  
 RA VALENS M., BOHN C., DAIGNAN-FORNIER B., DANG V., BOLOTIN-FUKUHARA M.;  
 RT "The sequence of a 54.7 kb fragment of yeast chromosome XV reveals the  
 RT presence of two tRNAs and 24 new open reading frames."  
 RL Yeast 13:379-390(1997).  
 DR EMBL: 274972: CAA99257.1; -  
 DR EMBL: 270678: CAA94549.1; -  
 DR PRAM: PF00628: PHD.1  
 SQ SEQUENCE 219 AA; 25350 MW; 1119F5E2 CRC32;

Query Match 41.8%; Score 61; DB 3; Length 219;  
 Best Local Similarity 47.1%; Pred. No. 7.28e+00;  
 Matches 8; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Db 12 DIRSFLSTLDHP-CE 27  
 : : : : :  
 QY 1 DVNYAFLLHATDLPACD 17

RESULT 12  
 ID 063211 PRELIMINARY; PRT; 223 AA.  
 AC 063211;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91062362.  
 RA BOND R.W., WYBORSKI R.J., GOTTLIEB D.I.;  
 RT "Developmentally regulated expression of an exon containing a stop  
 RT codon in the gene for glutamic acid decarboxylase."  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8771-8775(1990).  
 DR EMBL: M38350: AAA41185.1; -

DR PFAM: PF00282: pyridoxal dec; 1.  
 SQ SEQUENCE 223 AA; 25069 MW; C7162AC1 CRC32;  
 Query Match 41.8%; Score 61; DB 11; Length 223;  
 Best Local Similarity 47.4%; Pred. No. 7.28e+00;  
 Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Db 91 EIDFSNLFADLLPACDGE 109  
 : : : : :  
 QY 1 DVNYAFLLHATDLPACDGE 19

RESULT 13  
 ID 042504 PRELIMINARY; PRT; 236 AA.  
 AC 042504;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE HOMEBOX PROTEIN HOXC-6.  
 GN ERHXC-6.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;  
 OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 97285126.  
 RA APARICIO S., HAWKER K., COTTAGE A., MIKAWA Y., ZUO L., VENKATESH B.,  
 RA CHEN E., KRUMLAUF R., BRENNER S.;  
 RT "Organization of the Fugu rubripes Hox clusters: evidence for  
 RT continuing evolution of vertebrate Hox complexes."  
 RL Nat. Genet. 16:79-83(1997).  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: U92572: AAB68682.1; -  
 DR HSSP: P02833; 9ANT.  
 DR PROSITE: PS00027: HOMEBOX\_1; 1.  
 DR PFAM: PF00046: homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR PRINTS: PR00025; ANTENNAPEDIA.  
 KW Homeobox; DNA-binding; Nuclear  
 SQ SEQUENCE 236 AA; 27181 MW; 77DCC03C CRC32;

Query Match 41.8%; Score 61; DB 13; Length 236;  
 Best Local Similarity 54.5%; Pred. No. 7.28e+00;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 76 FLDKDVLPSC 86  
 : : : : :  
 QY 6 FLHATDLPAC 16

RESULT 14  
 ID 047099 PRELIMINARY; PRT; 254 AA.  
 AC 047099;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)  
 DE CS31A MINOR SUBUNIT PRECURSOR.  
 GN CLPL.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-R-12;  
 RA DER VARRANTAN M.;  
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U05182: AAA23586.1; -  
 DR SIGNAL.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 254 CS31A MINOR SUBUNIT.  
 SQ SEQUENCE 254 AA; 27021 MW; 6B28C6FD CRC32;

Query Match 41.8%; Score 61; DB 2; Length 254;  
 Best Local Similarity 63.6%; Pred. No. 7.28e+00;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 7 FLFASLLPSC 17  
 |||:|:|:|  
 QY 6 FLMATDLPAC 16

RESULT 15  
 ID Q41661 PRELIMINARY; PRT; 286 AA.  
 AC Q41661;  
 DT 01-NOV-1996 (TREMBLER, 01, Created)  
 DT 01-NOV-1996 (TREMBLER, 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLER, 12, Last annotation update)  
 DE PUTATIVE NARBONIN-LIKE 2S PROTEIN.  
 OS Vicia faba (Broad bean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;  
 OC core eudicots; Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae;  
 OC Vicia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=COTYLEDON;  
 RA NONG V.; SCHLESIER B.; MUENTZ K.;  
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z46834; CAA6875.1; -;  
 DR MENDEL; 16614; Vicia; 2552; 16614.  
 DR PRINTS; PR00551; 2SGLOBULIN.  
 SQ SEQUENCE 286 AA; 32575 MW; ABE3A19D CRC32;

Query Match 41.8%; Score 61; DB 10; Length 286;  
 Best Local Similarity 31.3%; Pred. No. 7.28e+00;  
 Matches 5; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Db 129 DINEYIKSDELFVNC 144  
 |||:|:|:|:|  
 QY 1 DVNTAFMATDLPAC 16

Search completed: Tue Mar 7 21:07:26 2000  
 Job time : 11 secs.

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MPerch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Mar 7 21:19:24 2000; Maspar time 3.17 Seconds  
 149,639 Million cell updates/sec  
 Tabular output not generated.

Title: >US-08-981-824-2  
 Description: (1-20) from US08981824.pep  
 Perfect Score: 159  
 Sequence: 1 SNMYAMTARFKMPEVKEK 20

Scoring table: PAM 150  
 Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 08  
 Listing first 45 summaries

Database: a-geneseq35  
 1:geneseqp

Statistics: Mean=20.912; Variance 73.027; scale 0.286

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	159	100.0	20	1 W01794	Human 65 kD glutamine	5.66e-09
2	159	100.0	20	1 W18843	65 kD glutamic acid de	5.66e-09
3	159	100.0	341	1 R59522	GAD65 1-244 N-terminal	5.66e-09
4	159	100.0	503	1 R23645	Human GAD65 gene produ	5.66e-09
5	159	100.0	540	1 R59520	GAD65 1-45 N-terminal	5.66e-09
6	159	100.0	344	1 R59524	GAD65 545-585 C-termin	5.66e-09
7	159	100.0	534	1 R59518	GAD65 1-31 deleted, C4	5.66e-09
8	159	100.0	584	1 W86017	Human GAD65 protein se	5.66e-09
9	159	100.0	584	1 W34519	Human GAD65 protein	5.66e-09
10	159	100.0	585	1 R79105	Human glutamic acid de	5.66e-09
11	159	100.0	585	1 R28766	Human pancreatic islet	5.66e-09
12	159	100.0	585	1 W35361	Human 65k-glutamic aci	5.66e-09
13	159	100.0	585	1 R29629	Human GAD 65.	5.66e-09
14	159	100.0	585	1 R59516	Human GAD65.	5.66e-09
15	159	100.0	585	1 W12402	65 kD human glutamic a	5.66e-09
16	159	100.0	585	1 R17641	Human GAD.	5.66e-09
17	155	97.5	20	1 R72277	Glutamic acid decarbox	1.57e-08
18	148	93.1	341	1 R59523	GAD65 1-244 N-terminal	9.32e-08
19	148	93.1	340	1 R59521	GAD65 1-45 N-terminal	9.32e-08
20	148	93.1	544	1 R59525	GAD65 545-585 C-termin	9.32e-08
21	148	93.1	554	1 R59519	GAD65 1-31 deleted, C4	9.32e-08
22	148	93.1	584	1 W86018	Rat GAD65 protein sequ	9.32e-08
23	148	93.1	584	1 W34520	Rat GAD65 protein.	9.32e-08

24	148	93.1	585	1 R23644	Rat GAD65 gene product	9.32e-08
25	148	93.1	585	1 R59517	Rat GAD65.	9.32e-08
26	148	93.1	585	1 R29628	Rat GAD 65.	9.32e-08
27	148	93.1	594	1 W74717	Amino acid sequence of	9.32e-08
28	148	93.1	605	1 R71733	Rat glutamic acid deca	9.32e-08
29	147	92.5	585	1 W14916	Modified glutamic acid	1.20e-07
30	147	92.5	585	1 W14915	Modified glutamic acid	1.20e-07
31	126	79.2	20	1 W10300	Mammalian GAD 65 pepti	2.32e-05
32	122	76.7	14	1 W18861	65 kD glutamic acid de	6.25e-05
33	122	76.7	14	1 R76653	Peptide derived from h	6.25e-05
34	121	76.1	23	1 R29627	GAD peptide.	8.00e-05
35	112	70.4	181	1 R27219	Islet GAD.	7.25e-04
36	112	70.4	593	1 R27220	Brain GAD #2.	7.25e-04
37	112	70.4	594	1 W74716	Amino acid sequence of	7.25e-04
38	112	70.4	594	1 R27221	Full length brain GAD.	7.25e-04
39	109	68.6	181	1 R27218	Brain GAD.	1.50e-03
40	103	64.8	594	1 R27222	Full length islet GAD.	6.38e-03
41	101	63.5	13	1 W35531	Glutamic acid decarbox	1.03e-02
42	91	57.2	506	1 W20064	Rat GADII protein.	1.10e-01
43	91	57.2	506	1 W22305	Rat GADII.	1.10e-01
44	87	54.7	493	1 W20065	Human GADII protein.	2.78e-01
45	87	54.7	493	1 W22306	Human GADII.	2.78e-01

## ALIGNMENTS

RESULT 1  
 ID W01794 standard; peptide: 20 AA.  
 AC W01794; (first entry)  
 DT 15-OCT-1997  
 DE Human 65 kD glutamine decarboxylase peptide.  
 KW Human 65 kD glutamine decarboxylase; GAD; diagnosis; predisposition;  
 KW tumour; immunological; disease; autoimmune; diabetes; reagent;  
 KW determination; T cell; subpopulation; medication; treatment;  
 KW prevention; production; antigen; immunogen; tolerogen; isolation;  
 KW rejection; inactivation.  
 OS Homo sapiens.  
 PN DE19525784-A1.  
 PD 16-JAN-1997.  
 PF 14-JUL-1995; 025784.  
 PR 14-JUL-1995; DE-025784.  
 PA (BOER) BOEHRINGER MANNHEIM GMBH.  
 PI Albert W, Boltard C, Endl J, Jung G, Schendel D;  
 PI Stahl P, Van Endert P;  
 DR WPI: 97-078452/08.  
 PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of  
 PT diabetes, etc.  
 PS Claim 1: Page 12; 15pp; German.  
 CC The present peptide is a fragment of the human 65 kD glutamine  
 CC decarboxylase (GAD), which can be used to diagnose, or diagnose a  
 CC predisposition to, a tumour or immunological disease, preferably an  
 CC autoimmune disease, especially diabetes. It can also be used as a  
 CC reagent to determine specific T cell subpopulations, in medicaments  
 CC to treat or prevent immunological diseases, preferably autoimmune  
 CC diseases, especially diabetes, to produce antigens, especially  
 CC immunogens or tolerogens and to isolate specific T cell  
 CC subpopulations, which can be used to produce antigens or for  
 CC reinjection, optionally after inactivation.  
 SQ Sequence 20 AA:  
 Query Match 100.0%; Score 159; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 SNMYAMTARFKMPEVKEK 20  
 QY 1 SNMYAMTARFKMPEVKEK 20  
 RESULT 2  
 ID W18843 standard; peptide: 20 AA.  
 AC W18843;  
 DT 05-JAN-1998 (first entry)

DE 65 kD glutamic acid decarboxylase peptide fragment II.  
 KW GAD: 65 kD: human: glutamic acid decarboxylase; autoreactive; diagnosis;  
 KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;  
 KW predisposition; autoimmune; tumour; rheumatoid arthritis;  
 KW multiple sclerosis.  
 OS Synthetic.  
 PN DE19526561-A1.  
 PD 23-JAN-1997.  
 PR 20-JUL-1995; 026561.  
 PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
 PI Donle F, Endl J, Ganz M, Jung G, Kientsch-engel R;  
 PI Pozzilli P, Stahl P;  
 DR WPI: 97-088254/09.  
 PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -  
 PT involving intradermal admn. of auto-reactive substances  
 PS Claim 11; Page 9; 12pp; German.  
 CC W18842-70 are peptide fragments of the 65 kD human glutamic acid  
 CC decarboxylase (GAD). The fragments are autoreactive substances used for  
 CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is  
 CC determined by using a claimed method for diagnosis of cell-mediated  
 CC diseases or a predisposition to cell-mediated diseases, which is effected  
 CC by administering an autoreactive substance intradermally and establishing  
 CC the diagnosis on the basis of the occurrence or lack of a positive  
 CC reaction at the site of administration. The method is used for diagnosis  
 CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases  
 CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 159; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 SNMYAMMIARFKMPPEVKEK 20  
 OY 1 SNMYAMMIARFKMPPEVKEK 20

RESULT 3  
 ID R59522 standard; protein: 341 AA.  
 AC R59522;  
 DT 09-NOV-1994 (first entry)  
 DE GAD65 1-244 N-terminal-deleted mutant.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody; mutagenesis.  
 OS Homo sapiens.  
 PN W09412529-A.  
 PD 09-JUN-1994.  
 PR 02-DEC-1993; U11705.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure; Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 341 AA;

Query Match 100.0%; Score 159; DB 1; Length 341;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 SNMYAMMIARFKMPPEVKEK 21  
 OY 1 SNMYAMMIARFKMPPEVKEK 20

RESULT 4  
 ID R23645 standard; Protein: 503 AA.  
 AC R23645;  
 DT 02-NOV-1992 (first entry)  
 DE Human GAD65 gene product.  
 KW Glutamic acid decarboxylase; IDDM; stiff man syndrome;  
 KW autoantibodies.  
 OS Homo sapiens.  
 PN W09205446-A.  
 PD 02-APR-1992.  
 PR 23-SEP-1991; 006872.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Erlander MG, Kaufman DL, Tobin AJ;  
 DR WPI: 92-150489/18.  
 DR N-RSDB: 024184.  
 PT Novel cDNA encoding GAD65 polypeptide - used to produce GAD65 for  
 PT therapeutic and diagnostic application in insulin-dependent  
 PT diabetes mellitus patients  
 PS Disclosure; Fig 3; 53pp; English.  
 CC The sequence given is a glutamic acid decarboxylase (GAD65). GAD65  
 CC can be used for the diagnosis and therapy of patients with autoimmune  
 CC diseases, esp. insulin-dependant diabetes mellitus (IDDM) and "stiff  
 CC man" syndrome. It is possible to use either the entire GAD65 protein  
 CC or polypeptide fragments of it for the immunological detection of  
 CC autoantibodies to GAD65 which are indicative of IDDM and other auto-  
 CC immune diseases. The production of this sequence by recombinant DNA  
 CC technology allows large scale production of eukaryotic GAD65 in its  
 CC native form without the need for separation from other proteinaceous  
 CC prods.  
 SQ Sequence 503 AA;

Query Match 100.0%; Score 159; DB 1; Length 503;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMMIARFKMPPEVKEK 265  
 OY 1 SNMYAMMIARFKMPPEVKEK 20

RESULT 5  
 ID R59520 standard; protein: 540 AA.  
 AC R59520;  
 DT 09-NOV-1994 (first entry)  
 DE GAD65 1-45 N-terminal-deleted mutant.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody; mutagenesis.  
 OS Homo sapiens.  
 PN W09412529-A.  
 PD 09-JUN-1994.  
 PR 02-DEC-1993; U11705.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure; Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 540 AA;

Query Match 100.0%; Score 159; DB 1; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;

Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
Db 201 SNMYAMMIARFKMPEYKER 220  
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QY 1 SNMYAMMIARFKMPEYKER 20

RESULT 6  
ID R59524 standard; protein: 544 AA.

AC R59524;  
DT 09-NOV-1994 (first entry)  
DE GAD65 545-585 C-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN MO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993: U11705.  
PR 03-DEC-1992: US-984935.  
PS (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp: English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. The C-terminally deleted mutants given in R59524-25  
CC are able to recognize IDDM autoantibodies having the specificity  
CC of MICAA/MICAF, but not those having the specificity of MICAI/MICAF3  
CC or MICAA. These mutants also have some N-terminal modifications  
CC to improve solubility.  
SQ Sequence 544 AA;

Query Match 100.0%; Score 159; DB 1; Length 544;  
Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Db 246 SNMYAMMIARFKMPEYKER 265  
|||||  
QY 1 SNMYAMMIARFKMPEYKER 20

RESULT 7  
ID R59518 standard; protein: 554 AA.  
AC R59518;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-31 deleted, C45A mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN MO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993: U11705.  
PR 03-DEC-1992: US-984935.  
PS (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp: English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 554 AA;

Query Match 100.0%; Score 159; DB 1; Length 554;

Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
Db 215 SNMYAMMIARFKMPEYKER 234  
|||||  
QY 1 SNMYAMMIARFKMPEYKER 20

RESULT 8  
ID W86017 standard; protein: 584 AA.

AC W86017;  
DT 22-FEB-1999 (first entry)  
DE Human GAD65 protein sequence.  
KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
insulin-dependent diabetes mellitus; stiff man syndrome.  
OS Homo sapiens.  
PN US5849506-A.  
PD 15-DEC-1998.  
PF 25-MAY-1995: 450755.  
PR 02-DEC-1993: US-161290.  
PR 03-DEC-1992: US-984935.  
PR 25-MAY-1995: US-450755.  
PS (REGC ) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 99-069720/06.  
PT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
PT diabetes and stiff man syndrome  
PS Examples: Fig 1; 31pp: English.  
CC This represents a human GAD65 protein sequence. The invention provides  
CC soluble fragments of GAD65 that are specifically reactive with at least  
CC one class of GAD65 autoantibody. The fragments are substantially free of  
CC N-terminal amino acids that would otherwise limit solubility. Different  
CC fragments contain different epitopes for different classes of GAD65  
CC autoantibodies. These fragments are used in the methods of the invention  
CC for detection of GAD65 autoantibodies. The methods are used for  
CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and  
CC stiff man syndrome.  
SQ Sequence 584 AA;

Query Match 100.0%; Score 159; DB 1; Length 584;  
Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Db 246 SNMYAMMIARFKMPEYKER 265  
|||||  
QY 1 SNMYAMMIARFKMPEYKER 20

RESULT 9  
ID W34519 standard; protein: 584 AA.  
AC W34519;  
DT 24-MAR-1998 (first entry)  
DE Human GAD65 protein.  
KW GAD65; glutamic acid decarboxylase protein; human; soluble fragment;  
autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
stiff man syndrome; therapy.  
OS Homo sapiens.  
PN US5691448-A.  
PD 25-NOV-1997.  
PF 02-DEC-1993: 161290.  
PR 02-DEC-1993: US-161290.  
PR 03-DEC-1992: US-984935.  
PS (BAEK/) BAEKESKOV S.  
PA (KIMJ/) KIM J.  
PA (NAMC/) NAMCHUK M.  
PA (RICH/) RICHTER W.  
PI Baekkeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 98-017711/02.  
PT Soluble fragments of glutamic acid decarboxylase GAD65 - used to  
PT distinguish between insulin-dependent diabetes mellitus and  
PT stiff-man syndrome  
PS Disclosure: column 27-30; 30pp: English.

CC This sequence represents the human glutamic acid decarboxylase protein  
 CC GAD65. The invention relates to soluble fragments of a GAD65 protein that  
 CC are specifically reactive with a GAD65 autoantibody (AAb), where the  
 CC fragment is at least 99% pure and the AAb binds to a conformational  
 CC epitope of the fragment. The soluble GAD65 fragments can be used to  
 CC distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff  
 CC man syndrome. They can also be used for diagnosis and treatment of IDDM  
 CC and stiff man syndrome. The fragments can distinguish different temporal  
 CC stages in the progression of IDDM.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 159; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKMPEVKEK 265  
 OY 1 SNMYAMTARFKMPEVKEK 20

RESULT 10  
 ID R79105 standard; Protein: 585 AA.  
 AC R79105:  
 DT 13-NOV-1995 (first entry)  
 DE Human glutamic acid decarboxylase (GAD65).  
 KW Rat glutamic acid decarboxylase; GAD65; autoimmune disorders;  
 KW insulin-dependent diabetes mellitus; stiff man disease.  
 OS Homo sapiens.  
 PN W09507992-A.  
 PD 23-MAR-1995.  
 PF 24-AUG-1984; U09478.  
 PR 17-SEP-1993; US-123859.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Cläre-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;  
 DR WPI: 95-131360/17.  
 DR N-PSDB: 086482.  
 PT New polypeptide fragments of glutamic acid decarboxylase - for  
 PT diagnosis and treatment of autoimmune disease, esp. insulin  
 PT dependent diabetes, also related nucleic acid, vectors,  
 PT antibodies, hybridoma(s) etc.  
 PS Example 1; Fig 3; 100pp; English.  
 CS 086481 and 086482 encode R17133 and R79105, rat and human glutamic  
 CC acid decarboxylase (GAD65) respectively, from which the GAD65  
 CC fragments described in R72261-R72298 were derived. These fragments  
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose  
 CC and treat GAD-related autoimmune disorders, such as insulin  
 CC dependent diabetes mellitus or stiff man disease.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKMPEVKEK 265  
 OY 1 SNMYAMTARFKMPEVKEK 20

RESULT 11  
 ID R28756 standard; Protein: 585 AA.  
 AC R28756:  
 DT 20-APR-1993 (first entry)  
 DE Human pancreatic islet cell glutamic acid decarboxylase.  
 KW GAD; insulin dependent diabetes melting; IDDM; autoantibody detection.  
 OS Homo sapiens.  
 PN W09220811-A.  
 PD 26-NOV-1992.  
 PF 14-MAY-1992; U04079.  
 PR 15-MAY-1991; US-702162.  
 PA (UNIM ) UNIV WASHINGTON.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Foster DC, Grubir CE, Hagopian W, Karlson AE, Lermack A, Ohara PJ;  
 DR WPI: 92-415789/50.

DR N-PSDB: Q31793.  
 PT Polynucleotide encoding human islet glutamic acid decarboxylase -  
 PT used to test for auto-antibodies against itself to diagnose  
 PT insulin dependent diabetes mellitus  
 PS Disclosure: Fig 2; 45pp; English.  
 CC The sequence is that of human pancreatic islet glutamic acid  
 CC decarboxylase (GAD) which is used to test biological samples for  
 CC the presence of autoantibodies to human GAD. It can also be used  
 CC to remove antibodies against GAD from plasma in order to treat an  
 CC autoimmune response to GAD, e.g. in insulin-dependent diabetes mellitus  
 CC (IDDM), and may also be used to induce immunological tolerance to GAD  
 CC by giving GAD that specifically binds the GAD receptor on immature T  
 CC or B cells.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKMPEVKEK 265  
 OY 1 SNMYAMTARFKMPEVKEK 20

RESULT 12  
 ID W35361 standard; Protein: 585 AA.  
 AC W35361:  
 DT 22-APR-1998 (first entry)  
 DE Human 65K-glutamic acid decarboxylase.  
 KW Mouse; human; glutamic acid decarboxylase; GAD65; diagnosis;  
 KW autoimmune reaction; T cell; mammalian skin; autoimmune disease;  
 KW insulin independent diabetes; inflammation.  
 OS Homo sapiens.  
 PN W09736618-A1.  
 PD 09-OCT-1997.  
 PE 31-MAR-1997; J01104.  
 PR 01-APR-1996; JP-078878.  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PI Kure S, Muto Y, Narisawa K, Sakata Y, Satoh J;  
 DR WPI: 97-502847/46.  
 PT Composition containing 65K-glutamic acid decarboxylase or its  
 PT partial peptide(s) - for diagnosing diseases associated with  
 PT autoimmune reaction  
 PS Claim 8; Page 14-16; 32pp; Japanese.  
 CS A composition has been developed for diagnosing diseases associated  
 CC with autoimmune reaction caused by 65K-glutamic acid decarboxylase  
 CC (GAD65) or its partial peptides. The composition reacts with T cells  
 CC in and/or on the surface of mammalian skin to cause inflammation.  
 CC The present sequence represents human GAD65. GAD65 and its partial  
 CC peptides are used to diagnose diseases associated with autoimmune  
 CC disease, e.g. insulin independent diabetes. The test is a very  
 CC simple skin test.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5,66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKMPEVKEK 265  
 OY 1 SNMYAMTARFKMPEVKEK 20

RESULT 13  
 ID R29629 standard; Protein: 585 AA.  
 AC R29629:  
 DT 05-MAY-1993 (first entry)  
 DE Human GAD 65.  
 KW Glutamic acid decarboxylase; auto immune disease; insulin dependent;  
 KW diabetes mellitus; drug screening; antibody; stiff man syndrome.  
 OS Homo sapiens.  
 PN EP-519469-A.  
 PD 23-DEC-1992.

PF 17-JUN-1992: 110308.  
 PR 18-JUN-1991: US-716909.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Claret-Salzier MJ, Erlander MG, Kaufman DL, Tobin AJ;  
 DR WPI; 92-425701/52.  
 N-PSDB: 032760.  
 PT Glutamic acid decarboxylase isolated polypeptide(s) - useful for  
 diagnosis and treatment of auto-immune diseases, e.g. insulin  
 dependent diabetes mellitus, drug screening and antibody prodn.  
 PS Disclosure: Fig 3; 35pp; English.  
 CC The DNA encoding glutamic acid decarboxylase (GAD 65) was obtd. by  
 CC standard recombinant DNA techniques. The protein, or fragments of  
 CC it, may be used for the detection of autoantibodies to GAD 65.  
 CC It can also be used for screening drugs such as those that alter  
 CC GAD function and for generation of antibodies which can be used to  
 CC detect GAD 65. Such methods can be used in the diagnosis and  
 CC therapy of autoimmune diseases such as insulin dependent diabetes  
 CC mellitus and "stiff man" syndrome. The protein can be used to bind  
 CC or block the continuance of an autoimmune response to GAD 65.  
 CC It may also be coupled to therapeutic agents and used immunothera-  
 CC peutically. See also R29625-8.  
 SQ Sequence 585 AA;  
 Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 246 SNMYAMMIAREKMPPEVKEK 265  
 OY 1 SNMYAMMIAREKMPPEVKEK 20  
 |||||

RESULT 14  
 ID R59516 standard; protein: 585 AA.  
 AC R59516:  
 DT 09-NOV-1994 (first entry)  
 DE Human GAD65  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 OS Homo sapiens.  
 PN MO9412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705  
 PR 03-DEC-1992; US-984935.  
 PA (REGC ) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI; 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure: Fig. 1; 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 585 AA;  
 Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 246 SNMYAMMIAREKMPPEVKEK 265  
 OY 1 SNMYAMMIAREKMPPEVKEK 20  
 |||||

KW 65 kD glutamic acid decarboxylase; human; GAD65; enzyme: pancreas;  
 KW neuron; central nervous system; type 1 diabetes; autoimmune response;  
 KW T cell; therapy.  
 OS Homo sapiens.  
 PN MO9700891-A1.  
 PD 09-JAN-1997.  
 PF 24-JUN-1996; U10790.  
 PR 23-JUN-1995; US-494624.  
 PA (KENN-) KENNEDY INST RHEUMATOLOGY.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES INC.  
 PA (SBAR-) ST BARTHOLOMEW'S HOSPITAL CENT CLINICAL.  
 PI Conlon PJ, Gaur A, Leslie RDG, Ling N, Londei M;  
 DR WPI; 97-087322/08.  
 N-PSDB: T61097.  
 PT New human glutamic acid decarboxylase peptide(s) - used for  
 PT treatment, diagnosis and determining predisposition to diabetes and  
 PT for ameliorating auto-immune responses.  
 PS Disclosure: Fig 1; 28pp; English.  
 CC This sequence represents the 65 kD isoform of human glutamic acid  
 CC decarboxylase (GAD65). GAD is an enzyme expressed in the beta cells of  
 CC the pancreas, and in neurons of the central nervous system. There are two  
 CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of  
 CC GAD65 have been identified in Type 1 diabetic patients. Fragments of  
 CC GAD65, and analogues of the fragments, are used in the methods of the  
 CC invention. The methods are for detecting or treating diabetes or a  
 CC predisposition to diabetes. The peptides can also be used for  
 CC ameliorating an autoimmune response in a patient. Alteration of the  
 CC native peptides with selective changes of crucial residues can induce  
 CC unresponsiveness or change the responsiveness of antigen-specific  
 CC autoreactive T cells. The peptide analogues compete for binding to MHC  
 CC and do not cause proliferation of the corresponding native  
 CC peptide-specific T cells.  
 SQ Sequence 585 AA;  
 Query Match 100.0%; Score 159; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 5.66e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 246 SNMYAMMIAREKMPPEVKEK 265  
 OY 1 SNMYAMMIAREKMPPEVKEK 20  
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#experimental_source pancreatic islet
REFERENCE
#authors
  Bu, D.F.; Tobin, A.J.
#journal
  Genomics (1994) 21:222-228
#title
  The exon-intron organization of the genes (GAD1 and GAD2)
  encoding two human glutamate decarboxylases (GAD-67 and
  GAD-65) suggests that they derive from a common ancestral
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  it has several isoforms, each encoded by a separate gene. GAD has
  also been implicated as an autoantigen in autoimmune disease
  stiff-man syndrome and insulin-dependent diabetes mellitus.
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    0; Mismatches
    0; Indels
    0; Gaps
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  1 SNNYAMLIARFKMFPEVK 20
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  14-Jul-1995 #text_change
  22-Jun-1999
DATE
  J04064
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  J04064
REFERENCE
  #journal
    Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
    Gene (1995) 152:257-260
  #title
    Sequences of two porcine glutamic acid decarboxylases (65-and
    67-kDa GAD).
#cross-references
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#accession
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  This enzyme catalyzes the conversion of glutamic acid into
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CLASSIFICATION
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KEYWORDS
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FEATURE
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    2; Length
    585;
  Matches
    19; Conservative
    1; Mismatches
    0; Indels
    0; Gaps
    0;
Db
  246 SNNYAMLIARFKMFPEVK 265
  1 SNNYAMLIARFKMFPEVK 20
  1 SNNYAMLIARFKMFPEVK 20
```

```
RESULT
  3
ENTRY
  I67412
#type
  fragment
TITLE
  65 kDa glutamate decarboxylase, brain - mouse (fragment)
#formal_name
  Mus musculus #common_name
  house mouse
#organism
  27-Feb-1997 #sequence_revision
  27-Feb-1997 #text_change
  30-May-1997
DATE
  I67412
ACCESSIONS
  I67412
REFERENCE
  153274
#authors
  Faulkner-Jones, B.E.; Gram, D.S.; Kun, J.; Harrison, L.C.
#journal
  Endocrinology (1993) 133:2962-2972
#title
  Localization and quantitation of expression of two glutamate
  decarboxylase genes in pancreatic beta-cells and other
  peripheral tissues of mouse and rat.
#cross-references
  M0ID:94062679
#accession
  I67412
#status
  preliminary; translated from GB/EMBL/DDBJ
#molecule_type
  mRNA
#residues
  1-205 #label
  RES
#cross-references
  GB:567454; NID:9456852
CLASSIFICATION
#superfamily
  human glutamate decarboxylase
SUMMARY
  #length
    205 #checksum
    3167
  Query Match
    Best Local Similarity
    93.1%; Score
    148; DB
    2; Length
    205;
  Matches
    18; Conservative
    2; Mismatches
    0; Indels
    0; Gaps
    0;
Db
  72 SNNYAMLIARFKMFPEVK 91
  1 SNNYAMLIARFKMFPEVK 20
  1 SNNYAMLIARFKMFPEVK 20
RESULT
  4
ENTRY
  JH0423
#type
  complete
TITLE
  glutamate decarboxylase (EC 4.1.1.15) 2 - rat
#formal_name
  Rattus norvegicus #common_name
  Norway rat
#organism
  31-Mar-1992 #sequence_revision
  23-Mar-1995 #text_change
  18-Jun-1999
DATE
  JH0423
ACCESSIONS
  JH0423
REFERENCE
  #journal
    Erlander, M.G.; Tillakaratne, N.J.K.; Feldblum, S.; Patel,
    N.; Tobin, A.J.
    Neuron (1991) 7:91-100
  #title
    Two genes encode distinct glutamate decarboxylases.
#cross-references
  M0ID:91299343
#accession
  JH0423
#molecule_type
  mRNA
#residues
  1-585 #label
  ERL
#cross-references
  GB:M72422; NID:9204225; PIDN:AAA63488.1; PID:9204226
#experimental_source
  brain
#note
  the authors translated the codon GAT for residue 86 as
  His, TCA for residue 198 as Ala, and CAG for residue
  428 as Trp
REFERENCE
  A60888
#authors
  Chang, Y.C.; Gottlieb, D.I.
#journal
  J. Neurosci. (1988) 8:2123-2130
#title
  Characterization of the proteins purified with monoclonal
  antibodies to glutamic acid decarboxylase.
#cross-references
  M0ID:88258610
#accession
  A60888
#status
  preliminary
#molecule_type
  protein
#residues
  'V',191-194,'X',196-203,'XX',206-219,'X',225-234,'X',
  236-247,'X',249-266,'X',524-537,539-543,'V',547-549,
  'X',551-553,'X',555-558 #label
  CHA
COMMENT
  This enzyme (GAD) catalyzes the formation of an inhibitory
  neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
  it has several isoforms, each encoded by a separate gene.
  #superfamily
  human glutamate decarboxylase
KEYWORDS
  carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
  phosphate
FEATURE
```



396 #binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 585 #molecular-weight 65402 #checksum 7756

Query Match 93.1%; Score 148; DB 1; Length 585;  
Best Local Similarity 90.0%; Pred. No. 1,11e-15;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMLIARKFPEVKEK 265  
|||||:|||||  
QY 1 SNMYAMLIARKFPEVKEK 20

RESULT 5  
ENTRY S38533 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - mouse  
ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 20-May-1994 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS S38533  
REFERENCE S38533  
#authors Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.  
#journal Biochim. Biophys. Acta (1993) 1216:157-160  
#title Cloning and sequence analysis of a murine cDNA encoding glutamate decarboxylase (GAD65).

#cross-references M0ID:94032481  
#accession S38533  
#status preliminary  
#molecule\_type mRNA  
#residues 1-585 #label LEE  
#cross-references GB:L16980; NID:g413867; PIDN:AAA93049.1; PID:g413868  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 396  
#binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 585 #molecular-weight 65224 #checksum 7599

Query Match 93.1%; Score 148; DB 1; Length 585;  
Best Local Similarity 90.0%; Pred. No. 1,11e-15;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMLIARKFPEVKEK 265  
|||||:|||||  
QY 1 SNMYAMLIARKFPEVKEK 20

RESULT 6  
ENTRY A46758 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - cat  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Felis silvestris catus #common\_name domestic cat  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS A46758; A45671  
REFERENCE A46758  
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.  
#submission submitted to GenBank, September 1989  
#accession A46758  
#molecule\_type mRNA  
#residues 1-594 #label KOB  
#cross-references GB:M18629; NID:g163858; PIDN:AAA51430.1; PID:g163859

REFERENCE A45671  
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.  
#journal J. Neurosci. (1987) 7:2768-2772  
#title Glutamic acid decarboxylase cDNA: nucleotide sequence encoding an enzymatically active fusion protein.  
#cross-references M0ID:87310623

#accession A45671  
#molecule\_type mRNA  
#residues 1-558, 'RGTRPFGWSSRITQLHSPIITSSSR' #label KO2  
#note this sequence has been revised in reference A46758  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS  
#gene GAD1  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 405  
#binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 594 #molecular-weight 66824 #checksum 5630

Query Match 73.0%; Score 116; DB 1; Length 594;  
Best Local Similarity 70.0%; Pred. No. 4.89e-09;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 255 SNMYSIMAARKFPEVKT 274  
|||||:|||||  
QY 1 SNMYSIMAARKFPEVKT 20

RESULT 7  
ENTRY I53274 #type fragment  
TITLE glutamate decarboxylase, 67K, brain - mouse (fragment)  
ORGANISM #formal\_name Mus sp. #common\_name mouse  
DATE 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 16-Feb-1997

ACCESSIONS I53274  
REFERENCE I53274  
#authors Faulkner-Jones, B.E.; Cram, D.S.; Kun, J.; Harrison, L.C.  
#journal Endocrinology (1993) 133:2962-2972  
#title Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat.

#cross-references M0ID:94062679  
#accession I53274  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type mRNA  
#residues 1-206 #label RES  
#cross-references GB:S67453; NID:g456853  
CLASSIFICATION #superfamily human glutamate decarboxylase  
SUMMARY #length 206 #checksum 3323

Query Match 70.4%; Score 112; DB 2; Length 206;  
Best Local Similarity 70.0%; Pred. No. 3.06e-08;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 57 SNMYSIMAARKFPEVKT 76  
|||||:|||||  
QY 1 SNMYSIMAARKFPEVKT 20

RESULT 8  
ENTRY S61534 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 62K isoform - mouse  
ALTERNATE\_NAMES glutamic acid decarboxylase  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 22-Jun-1999

ACCESSIONS S61534; S61533  
REFERENCE S61534  
#authors Katatova, Z.; Szabo, G.; Mugnai, E.; Greenspan, R.J.  
#journal Eur. J. Neurosci. (1990) 2:190-202  
#title Molecular identification of the 62 kd form of glutamic acid decarboxylase from the mouse.  
#accession S61534  
#molecule\_type mRNA  
#residues 1-585 #label KAT

```
##cross-references EMBL:249976
##experimental_source brain
REFERENCE
#authors Szabo, G.
#submission submitted to the EMBL Data Library, June 1995
#accession S61533
#molecule_type mRNA
#residues 1-554, 'YQPGDKANFRVYISNPAASQSDIDFLEIRLGODL' ##label
#cross-references EMBL:249976; NID:g886686; PIDN:CAA90277.1;
#experimental_source brain
#note the differences at the carboxyl end are due to a
frameshift error
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 585 #molecular-weight 65381 #checksum 5716

Query Match 70.4%; Score 112; DB 2; Length 585;
Best Local Similarity 70.0%; Pred. No. 3.06e-08;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 254 SNMYTMMARKYKPEVVK 273
Oy 1 SNMYTMMARKYKPEVVK 20

RESULT 9
ENTRY A41367 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - rat
ALTERNATE_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 12-Jun-1992 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999

ACCESSIONS A41367; A43756; JH0195
REFERENCE A41367
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;
Dyrberg, T.; Madsen, O.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
#title Cloning, characterization, and autoimmune recognition of rat
islet glutamic acid decarboxylase in insulin-dependent
diabetes mellitus.
#cross-references MUID:92020930
#accession A41367
#status preliminary
#molecule_type mRNA
#residues 1-593 #label MIC
REFERENCE ##cross-references GB:M76177; NID:g204227; PIDN:AAA4184.1; PID:g204228
#authors Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.
#journal Brain Res. Mol. Brain Res. (1990) 8:193-198
#title Characterization of a cDNA coding for rat glutamic acid
decarboxylase.
#cross-references MUID:91014554
#accession A43756
#status preliminary
#molecule_type mRNA
#residues 1-593 #label WYB
#cross-references GB:X57573; NID:g56183; PIDN:CAA4080.1; PID:g56184
#note the authors translated the codon TGT for residue 412 as
Ser and TCT for residue 413 as Cys

REFERENCE JH0195
#authors Julien, J.F.; Samama, P.; Maillet, J.
#journal J. Neurochem. (1990) 54:703-705
#title Rat brain glutamic acid decarboxylase sequence deduced from a
cloned cDNA.
#cross-references MUID:90132703
#accession JH0195
#molecule_type mRNA
#residues 1-102, 'V', '104-283', 'S', '285-286', 'AD', '289-343', 'EA', '346', 'I',
'348-351', 'LE', '354-379', 'R', '381-593' ##label JUL
#cross-references GB:X57572; NID:g56185; PIDN:CAA4080.1; PID:g56186
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
```

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neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE 404
#binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
SUMMARY #length 593 #molecular-weight 66640 #checksum 3971

Query Match 70.4%; Score 112; DB 1; Length 593;
Best Local Similarity 70.0%; Pred. No. 3.06e-08;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 254 SNMYTMMARKYKPEVVK 273
Oy 1 SNMYTMMARKYKPEVVK 20

RESULT 10
ENTRY S48135 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change
07-May-1999

ACCESSIONS S48135
REFERENCE S48135
#authors Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.;
Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.
#journal Ann. Hum. Genet. (1992) 56:255-265
#title Nucleotide sequence and chromosomal assignment of a cDNA
encoding the large isoform of human glutamate
decarboxylase.
#cross-references MUID:93080286
#accession S48135
#molecule_type mRNA
#residues 1-593 #label KEL
#cross-references EMBL:227550
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 593 #molecular-weight 66952 #checksum 4836

Query Match 70.4%; Score 112; DB 2; Length 593;
Best Local Similarity 70.0%; Pred. No. 3.06e-08;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 254 SNMYTMMARKYKPEVVK 273
Oy 1 SNMYTMMARKYKPEVVK 20

RESULT 11
ENTRY S51776 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
16-Feb-1997

ACCESSIONS S51776
REFERENCE S51775
#authors Johnstone, A.
#submission submitted to the EMBL Data Library, May 1993
#accession S51776
#status preliminary
#molecule_type mRNA
#residues 1-593 #label JOH
#cross-references EMBL:227550
#note this is an unpublished revision to the sequence from
reference S48135
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 593 #molecular-weight 66946 #checksum 4842

Query Match 70.4%; Score 112; DB 2; Length 593;
```

Best Local Similarity 70.0%; Pred. No. 3.06e-08;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 254 SNMYSIMARKYKPEVKTR 273  
||||:|||||  
QY 1 SNMYSIMARKYKPEVKER 20

RESULT 12  
ENTRY B41935 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS B41935; JH0805; JH0806; A61406; PQ0157; PQ0158; B41367; A36463; A54778 A41935

REFERENCE A41935  
#authors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.; Kautman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.  
#cross-references MUID:92196068  
#accession B41935  
#molecule\_type mRNA  
#residues 1-594 ##label BU1  
#cross-references GB:M81883; NID:g182935; PIDN:AAA62368.1; PID:g182936  
##experimental\_source pancreatic islet  
##note Sequence extracted from NCBI backbone (NCBIP:88006)

REFERENCE JH0805  
#authors Kawasaki, E.; Moriyuchi, R.; Watanabe, M.; Saitoh, K.; Charles Brunickard, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.; Akazawa, S.; Miyamoto, T.; Nagataki, S.  
#journal Biochem. Biophys. Res. Commun. (1993) 192:1353-1359  
#title Cloning and expression of large isoform of glutamic acid decarboxylase from human pancreatic islet.  
#cross-references MUID:93282845  
#accession JH0805  
##molecule\_type mRNA  
#residues 1-17 'N', 19-30, 'N', 32-67, 'K', 68-115, 'L', 117-154, 'T', 156-301, 'C', 303, 476, 'G', 478-491, 'G', 493-594 ##label KAW

REFERENCE #cross-references GB:561898; NID:g385310; PIDN:AAB26938.1; PID:g385311  
##experimental\_source pancreatic islet  
#authors Yamashita, K.; Cram, D.S.; Harrison, L.C.  
#journal Biochem. Biophys. Res. Commun. (1993) 192:1347-1352  
#title Molecular cloning of full-length glutamic acid decarboxylase 67 from human pancreas and islets.  
#cross-references MUID:93282844  
#accession JH0806  
##molecule\_type mRNA  
#residues 1-67, 'K', 68-435, 'L', 437-511, 'S', 513-594 ##label YAM

REFERENCE #cross-references GB:561897; NID:g385450; PIDN:AAB26937.1; PID:g385451  
##experimental\_source pancreatic islet  
#authors Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.  
#journal Lancet (1991) 338:1468-1469  
#title Cloning of large isoform of human brain glutamic acid decarboxylase.  
#cross-references MUID:92065769  
#accession A61406  
##molecule\_type mRNA  
#residues 62-67, 'K', 69-205, 'N', 207-564, 'L', 566-594 ##label KEL

REFERENCE #experimental\_source brain  
PQ0157  
#authors Cram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C.  
#journal Biochem. Biophys. Res. Commun. (1991) 176:1239-1244  
#title Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets.  
#cross-references MUID:91248209

#accession PQ0157  
##molecule\_type mRNA  
#residues 218-463 ##label CRI  
#cross-references GB:M70434  
##experimental\_source brain  
#accession PQ0158  
##molecule\_type mRNA  
#residues 218-234, 'K', 236-240, 'N', 242-288, 'H', 290-323, 'L', 325-329, 'D', 331-338, 'L', 340-390, 'S', 392-397 ##label CR2

REFERENCE #cross-references GB:M70435; NID:g182941; PIDN:AAA52513.1; PID:g182942  
##experimental\_source pancreatic islet  
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.; Dyberg, T.; Madsen, O.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
#title Cloning, characterization, and autoimmune recognition of rat islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.  
#cross-references MUID:92020930  
#accession B41367  
##molecule\_type mRNA  
#residues 317-482, 'R', 484-594 ##label MIC

REFERENCE A36463  
#authors Persson, H.; Pelto-Huikko, M.; Metsis, M.; Soeder, O.; Brene, S.; Skog, S.; Hoekfelt, T.; Ritzén, E.M.  
#journal Mol. Cell. Biol. (1990) 10:4701-4711  
#title Expression of the neurotransmitter-synthesizing enzyme glutamic acid decarboxylase in male germ cells.  
#cross-references MUID:90355986  
#accession A36463  
##molecule\_type mRNA  
#residues 527-594 ##label PER

REFERENCE #cross-references GB:M55574; NID:g182929; PIDN:AA72938.1; PID:g182930  
A54778  
#authors Bu, D.F.; Tobin, A.J.  
#journal Genomics (1994) 21:222-228  
#title The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral GAD.

#cross-references MUID:94375018  
#contents Intron-exon organization  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene. GAD has also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.

GENETICS  
#gene GDB:GAD1; GAD  
#cross-references GDB:119244; OMIM:266100  
#map\_position 2q31-2q31  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS alternative splicing; carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 405  
#binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted

SUMMARY #length 594 #molecular\_weight 66924 #checksum 6189

Query Match 70.4%; Score 112; DB 1; Length 594;  
Best Local Similarity 70.0%; Pred. No. 3.06e-08;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 255 SNMYSIMARKYKPEVKTR 274  
||||:|||||  
QY 1 SNMYSIMARKYKPEVKER 20

RESULT 13  
ENTRY JC4065 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 67k chain - pig  
ORGANISM #formal\_name Sus scrofa domestica #common\_name domestic pig  
DATE 30-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change

```

22-Jun-1999
ACCESSIONS JCA065
REFERENCE JCA064
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuna, M.
#journal Gene (1995) 152:257-260
#title Sequences of two porcine glutamic acid decarboxylases (65-and 67-kDa GAD).
#cross-references MIMD:95137399
#accession JCA065
##molecule-type mRNA
##residues 1-594 #label SUZ
##cross-references DDBJ:D31849; NID:g790966; PIDN:BA06636.1;
PID:d1007208; PID:g790967
##experimental-source brain
COMMENT This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS #superfamily human glutamate decarboxylase
FEATURE carbon-carbon lyase; carboxy-lyase
402-405 #domain DOPA decarboxylase binding #status predicted
#label B1N
#length 594 #molecular-weight 66894 #checksum 5491
SUMMARY
Query Match 70.4%; Score 112; DB 2; Length 594;
Best Local Similarity 70.0%; Pred. No. 3,06e-08;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 255 SNNYSIMARKYKYPPEVKTK 274
||||:|11:|11111|
QY 1 SNNYAMMIARFKMPEVKEK 20
RESULT 14
ENTRY S51775 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Jul-1995 #sequence_revision 21-Jul-1995 #extl_change 22-Jun-1999
ACCESSIONS S51775
REFERENCE Johnstone, A.
#authors submitted to the EMBL Data Library, May 1993
#submission S51775
#accession preliminary
##status
##molecule-type mRNA
##residues 1-594 #label JOH
##cross-references EMBL:Z22750; NID:g298098; PIDN:CAA80435.1;
PID:g298099
CLASSIFICATION #superfamily human: glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 594 #molecular-weight 66973 #checksum 6437
Query Match 70.4%; Score 112; DB 2; Length 594;
Best Local Similarity 70.0%; Pred. No. 3,06e-08;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Db 255 SNNYSIMARKYKYPPEVKTK 274
||||:|11:|11111|
QY 1 SNNYAMMIARFKMPEVKEK 20
RESULT 15
ENTRY S71489 #type complete
TITLE sulfoalanine decarboxylase (EC 4.1.1.29) - rat
ALTERNATE_NAMES cysteine sulfinate decarboxylase; cysteine sulfinic acid decarboxylase
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 09-Dec-1997 #sequence_revision 09-Dec-1997 #extl_change 22-Jun-1999
ACCESSIONS S71489; S78208; S55689; S55690
REFERENCE S71489
#authors Raymond, I.; Sergeant, A.; Tappaz, M.
#journal Biochim. Biophys. Acta (1996) 1307:152-156

```

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#title      Molecular cloning and sequence analysis of the cDNA encoding
            rat liver cysteine sulfinatase decarboxylase (CSD).
#cross-references NID:96283809
#accession  S71489
#molecule_type mRNA
#residues   1-493 ##label REV
##cross-references EMBL:X94155; NID:g1263163; PIDN:CAA63868.1;
            PID:e2184415; PID:g1263164
##experimental_source liver
#accession  S78208
#molecule_type protein
#residues   9-22;106-124;467-484 ##label REM
REFERENCE
#authors    Katsakia, P.J.; Jenkins, A.A.; Goodspeed, D.C.; Steele, R.D.
#journal     Biochim. Biophys. Acta (1995) 1262:79-82
#title       Cloning and characterization of rat cysteine sulfinic acid
            decarboxylase.
#cross-references NID:95290499
#note        the author's name has been corrected in reference S60723
#accession  S55689
##molecule_type mRNA
#residues   1-177, 'V', 179-457, 'W', 459, 'PCPTSEEMWPPPIYSRPT' ##label
            KAI
##cross-references EMBL:M4755; NID:g847652; PIDN:AAC42063.1;
            PID:g847653
#accession  S55690
##status     preliminary
#molecule_type protein
#residues    220-230 ##label KA2
REFERENCE
#authors     Katsaki, P.J.; Jenkins, A.A.; Goodspeed, D.C.; Steele, R.D.
#journal      Biochim. Biophys. Acta (1995) 1263:179
#contents     annotation: erratum
#note         this a correction of the author's name from reference S55689
CLASSIFICATION
#superfamily human glutamate decarboxylase
KEYWORDS       carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
            phosphate
FEATURE
305
            #binding_site pyridoxal phosphate (lys) (covalent)
305            #status predicted
SUMMARY
#length 493 #molecular_weight 55248 #checksum 7887
Query Match      57.2%; Score 91; DB 2; Length 493;
Best local similarity 50.0%; Pred. No. 3.18e-04;
Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Db 155 SNNATNLARFQRYPDCKOR 174
      |||||:||||:|:|:|:
      1 SNNATMMIARFKMFPEYKEX 20

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RL  Eur. J. Biochem. 212:597-603(1993).
CC  -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC  -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC  -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC  DECARBOXYLASE.
CC  -----
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CC  entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: M81882; AAA63267.1; -.
DR  EMBL: M74826; AAA58491.1; -.
DR  EMBL: X69936; CAA49554.1; ALT-INT.
DR  EMBL: M70435; AAA52513.1; -.
DR  PIR: A41292; A41292.
DR  PIR: P00158; P00158.
DR  MIM: 138275; -.
DR  PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR  PfAM: PF00282; Pyridoxal_dcc; 1.
KW  Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW  Pyridoxal phosphate; Multigene family.
FT  BINDING 396 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT  SEQUENCE 585 AA; 65411 MW; 8AD62862 CRC32;
SQ
Query Match 100.0%; Score 159; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 5,32e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNRYAMMTARFKMPPEVK 265
Qy 1 SNRYAMMTARFKMPPEVK 20
|||||
RESULT 2 STANDARD: PRT: 585 AA.
AC P48321:
DC 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 kd ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 kd GLUTAMIC ACID DECARBOXYLASE).
GN GAD2 OR GAD65.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RC MEDLINE: 95137399.
RA SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
RT "Sequences of two porcine glutamic acid decarboxylases (65- and
RT 67-kDa GAD)";
RL Gene 152:257-260(1995).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
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CC      EMBL, D31848; BA006635.1; -; HDC_YDC; 1.
DR      PROSITE, PS00392; DDC_GAD_HDC_YDC; 1.
DR      PFM: PF00282; pyridoxal_dec; 1.
KW      Neurotransmitter biosynthesis; Lyase: Decarboxylase;
KW      Pyridoxal phosphate; Multigene family.
FT      BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ      SEQUENCE 585 AA; 65388 MW; F3E9BD88 CRC32;

Query Match 95.6%; Score 152; DB 1; Length 585;
Best Local Similarity 95.0%; Pred. No. 2,806-19;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMTARFKMPEVKEK 265
0Y 1 SNMYAMTARFKMPEVKEK 20
|||||:|||||
RESULT 3
ID DCE2_MOUSE STANDARD; PRT; 585 AA.
AC P48320; O35519;
DI 01-FEB-1996 (Rel. 33, Created)
DI 01-FEB-1996 (Rel. 33, Last sequence update)
DI 15-JUL-1998 (Rel. 36, Last annotation update)
DI GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
DE GAD2 OR GAD65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-BRAIN;
RX MEDLINE: 94032481.
RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;
RT "Cloning and sequence analysis of a murine cDNA encoding glutamate
RT decarboxylase (GAD65)."
RL Biochim. Biophys. Acta 1216:157-160(1993).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6; TISSUE-BRAIN;
RX MEDLINE: 97115675.
RA ASADA H., KANAMURA Y., MARYAMA K., KUME H., DING R.G., JI F.Y.,
RA KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.;
RT "Gad65 lacking the 65 kDa isoform of glutamic acid decarboxylase
RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but
RT are susceptible to seizures."
RL Biochem. Biophys. Res. Commun. 229:891-895(1996).
RL [3]
RP SEQUENCE OF 175-379 FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 94062679.
RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;
RT "Localization and quantitation of expression of two glutamate
RT decarboxylase genes in pancreatic beta-cells and other peripheral
RT tissues of mouse and rat."
RL Endocrinology 133:2962-2972(1993).
CC - FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC - CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC - C- SUBUNIT: PYRIDOXAL PHOSPHATE.
CC - SIMILARITY: HOMODIMER (BY SIMILARITY).
CC - SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC DECARBOXYLASE.
CC
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CC
CC EMBL: L16980; AAA93049.1; -

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DR EMBL: D42051: BAA22893.1: -
DR EMBL: S67454: CAB32806.1: -
DR MGI: 95634; GAD2.
DR PROSITE: PS00392: DDC_GAD_HDC_YDC: 1.
DR PFAM: PF00282: Pyridoxal dec: 1.
KW Neurotransmitter biosynthesis; Lyase: Decarboxylase;
KW Pyridoxal phosphate; Multigene family: Decarboxylase;
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT CONFLICT 259 259 F -> S (IN REF. 2).
FT CONFLICT 319 319 I -> S (IN REF. 3).
FT CONFLICT 325 325 K -> E (IN REF. 2).
FT CONFLICT 499 499 P -> S (IN REF. 2).
FT SEQUENCE 585 AA: 65224 MW: 9855088 CRC32:

Query Match 93.1%; Score 148; DB 1; Length 585;
Best Local Similarity 90.0%; Pred. No. 2,65e-18;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMLIARKMPEVKEK 265
OY 1 SNMYAMLIARKMPEVKEK 20

RESULT 4
ID DCE2_RAT STANDARD: PRT: 585 AA.
AC Q05683;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD2 OR GAD65.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HIPOCAMPUS;
RA ERLANDER M.G., TILAKARATNE N.J., FELDBLUM S., PATEL N.,
RA TOBIN A.J.;
RT "Two genes encode distinct glutamate decarboxylases.";
RL Neuron 7:91-100(1991).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC DECARBOXYLASE.
CC -----
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CC -----
CC EMBL: M72422: AAA63488.1: -
DR PROSITE: PS00392: DDC_GAD_HDC_YDC: 1.
DR PFAM: PF00282: Pyridoxal dec: 1.
KW Neurotransmitter biosynthesis; Lyase: Decarboxylase;
KW Pyridoxal phosphate; Multigene family: Decarboxylase;
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT SEQUENCE 585 AA: 65402 MW: 8350601A CRC32:

Query Match 93.1%; Score 148; DB 1; Length 585;
Best Local Similarity 90.0%; Pred. No. 2,65e-18;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 246 SNMYAMLIARKMPEVKEK 265
OY 1 SNMYAMLIARKMPEVKEK 20

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RESULT 5
ID DCE1_FELCA STANDARD: PRT: 594 AA.
AC P14748;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OCCIPITAL CORTEX;
RX MEDLINE: 87310623
RA KOBAYASHI Y., KAUFMAN D.L., TOBIN A.J.;
RT "Glutamic acid decarboxylase cDNA: nucleotide sequence encoding an
RT enzymatically active fusion protein.";
RL J. Neurosci. 7:2768-2772(1987).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
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CC -----
CC EMBL: M18629: AAA51430.1: -
DR PIR: A45671; A45671.
DR PIR: A46758; A46758.
DR PROSITE: PS00392: DDC_GAD_HDC_YDC: 1.
DR PFAM: PF00282: Pyridoxal dec: 1.
KW Neurotransmitter biosynthesis; Lyase: Decarboxylase;
KW Pyridoxal phosphate; Multigene family: Decarboxylase;
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT SEQUENCE 594 AA: 66824 MW: 3820778 CRC32:

Query Match 73.0%; Score 116; DB 1; Length 594;
Best Local Similarity 70.0%; Pred. No. 9,26e-11;
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 255 SNMYSIMARKMPEVKT 274
OY 1 SNMYSIMARKMPEVKT 20

RESULT 6
ID DCE1_MOUSE STANDARD: PRT: 593 AA.
AC P48318;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA KARAROVA Z., SZABO G., MUGNAINI E., GREENSPAN R.;
RT "Molecular identification of the 62 kd form of glutamic acid

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RT decarboxylase from the mouse."  
RL Eur. J. Neurosci. 2:190-202(1990).  
RN [2]  
RP SEQUENCE OF 198-403 FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE: 94062679.  
RA FAULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.;  
RT "Localisation and quantitation of expression of two glutamate  
RT decarboxylase genes in pancreatic beta-cells and other peripheral  
RT tissues of mouse and rat."  
RT Endocrinology 133:2962-2972(1993).  
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
CC -1- CORYCTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
CC TYROC).  
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CC -----  
CC EMBL: 249976; CAA90277.1; -  
DR EMBL: S67453; CAB32805.1; -  
DR MGI: 95632; GAD1.  
DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
DR PFAM: PF00282; pyridoxal\_dec; 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family.  
FT BINING 404  
FT CONFLICT 234 E -> K (IN REF. 2).  
FT CONFLICT 258 S -> T (IN REF. 1).  
FT CONFLICT 360 D -> S (IN REF. 1).  
SQ SEQUENCE 593 AA; 66584 MW; 63BC57AA CRC32;  
  
Query Match 70.4%; Score 112; DB 1; Length 593;  
Best Local Similarity 70.0%; Pred. No. 7.41e-10;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Db 254 SNNYSIMARIKFFPEVKR 273  
QY 1 SNNYSIMARIKFFPEVKER 20  
||||:|||||  
  
RESULT 7  
ID DCEL\_RAT STANDARD; PRT; 593 AA.  
AC P18088;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
GN GAD1 OR GAD67.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 91014554.  
RA WYBORSKI R.J., BOND R.W., GOTTLEB D.I.;  
RT "Characterization of a cDNA coding for rat glutamic acid  
RT decarboxylase".  
RL Brain Res. Mol. Brain Res. 8:193-198(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 90132703.  
RA JULIEN J.F., SAMAMA P., MALLET J.;  
RT "Rat brain glutamic acid decarboxylase sequence deduced from a cloned  
RT cDNA.";

RL J. Neurochem. 54:703-705(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 92020930.  
RA MICHELSEN B.K., PETERSEN J.S., BOEL E., MOLDROP A., DYBERG T.,  
RA MADSEN O.D.;  
RT "Cloning, characterization, and autoimmune recognition of rat islet  
RT glutamic acid decarboxylase in insulin-dependent diabetes mellitus".  
RT Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).  
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
CC -1- CORYCTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMODIMER.  
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
CC TYROC).  
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CC -----  
CC EMBL: M34445; AAC42037.1; -  
DR EMBL: X57572; CAA40800.1; -  
DR EMBL: X57573; CAA40801.1; -  
DR EMBL: M76177; AAA41184.1; -  
DR PIR: A41367; A41367.  
DR PIR: A43756; A43756.  
DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
DR PFAM: PF00282; pyridoxal\_dec; 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family.  
FT BINING 404  
FT CONFLICT 103 L -> V (IN REF. 2).  
FT CONFLICT 284 E -> S (IN REF. 2).  
FT CONFLICT 287 EH -> AD (IN REF. 2).  
FT CONFLICT 344 AG -> EA (IN REF. 2).  
FT CONFLICT 347 T -> I (IN REF. 2).  
FT CONFLICT 352 FD -> LE (IN REF. 2).  
FT CONFLICT 380 L -> R (IN REF. 2).  
SQ SEQUENCE 593 AA; 66640 MW; 5A0B67C0 CRC32;  
  
Query Match 70.4%; Score 112; DB 1; Length 593;  
Best Local Similarity 70.0%; Pred. No. 7.41e-10;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
Db 254 SNNYSIMARIKFFPEVKR 273  
QY 1 SNNYSIMARIKFFPEVKER 20  
||||:|||||  
  
RESULT 8  
ID DCEL\_HUMAN STANDARD; PRT; 594 AA.  
AC Q99259;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
GN GAD1 OR GAD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 92196068.  
BU D.-F., ERLANDER M.G., HITZ B.C., TILAKARATNE N.J., KAUFMAN D.L.,  
RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;  
RT "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are  
RT each encoded by a single gene.";



Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).

[2] SEQUENCE FROM N.A.

RA MEDLINE: 94375018.

RA BU D.-F., TOBIN A.J.;

"The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD67 and GAD65) suggests that they derive from a common ancestral GAD.";

Genomics 21:222-228(1994).

[3] SEQUENCE FROM N.A.

RA TISSUE-BRAIN;

MEDLINE: 93060286.

RA KELLY C.D., EDWARDS Y., JOHNSTONE A.P., HARFEST E., NOGRADI A., NUSSLEY S.S., POVEY S., CARTER N.D.;

"Nucleotide sequence and chromosomal assignment of a cDNA encoding the large isoform of human glutamate decarboxylase.";

Ann. Hum. Genet. 56:255-265(1992).

[4] SEQUENCE FROM N.A.

RA MEDLINE: 93282844.

RA YAMASHITA K., CRAM D.S., HARRISON L.C.;

"Molecular cloning of full-length glutamic acid decarboxylase 67 from human pancreas and islets.";

Biochem. Biophys. Res. Commun. 192:1347-1352(1993).

[5] SEQUENCE FROM N.A.

RA TISSUE-PANCREATIC ISLETS;

MEDLINE: 93282845.

RA KAMAGAKI E., MORIUCHI R., MATANABE M., SATOH K., BRUNICARDI F.C., WATT P.C., YAMAGUCHI T., MULLEN Y., AKAZAWA S., MIYAMOTO T.;

"Cloning and expression of large isoform of glutamic acid decarboxylase from human pancreatic islet.";

Biochem. Biophys. Res. Commun. 192:1353-1359(1993).

[6] SEQUENCE FROM N.A.

RA GIORDA R., PEAKMAN M., VERGANI D., TRUCCO M.;

Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.

[7] SEQUENCE OF 218-397 FROM N.A.

RA TISSUE-BRAIN;

MEDLINE: 91248209.

RA CRAM D.S., BARRETT L.D., JOSEPH J.L., HARRISON L.C.;

"Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets.";

Biochem. Biophys. Res. Commun. 176:1239-1244(1991).

[8] SEQUENCE OF 527-594 FROM N.A.

RA TISSUE-TESTIS;

MEDLINE: 90353986.

RA PERSSON H., PELTO-HUIKKO M., METSIS M., SOEDER O., BRENE S., SKOG S., HOEKFELT T., RITZEN E.M.;

"Expression of the neurotransmitter-synthesizing enzyme glutamic acid decarboxylase in male germ cells.";

Mol. Cell. Biol. 10:4701-4711(1990).

CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.

CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + CO(2).

CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -1- SUBUNIT: HOMODIMER.

CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).

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CC EMBL: M81883: AAA62368.1: -

CC EMBL: L16888: AAB59427.1: -

CC EMBL: 222750: CAA80435.1: -

DR EMBL: S61897: AAB26937.1: -

DR EMBL: S61896: AAB26938.1: -

DR EMBL: M86522: AAA35900.1: -

DR EMBL: M70434: AAA5512.1: -

DR EMBL: M55574: AAA72938.1: -

DR EMBL: A28074: CAA01913.1: -

DR PIR: P00157: P00157.

DR MIM: 266100: -

DR PROSITE: PS00392: DDC-GAD-HDC\_YDC: 1.

DR PFM: PF00282: pyridoxal\_dec: 1.

KM Neurotransmitter biosynthesis: Lyase; Decarboxylase:

KW pyridoxal phosphate; Multigene family.

FT BINDING 405 405

FT CONFLICT 9 9

FT CONFLICT 16 17

FT CONFLICT 17 17

FT CONFLICT 18 18

FT CONFLICT 31 31

FT CONFLICT 68 68

FT CONFLICT 116 116

FT CONFLICT 136 136

FT CONFLICT 140 140

FT CONFLICT 142 142

FT CONFLICT 155 155

FT CONFLICT 206 206

FT CONFLICT 302 302

FT CONFLICT 436 436

FT CONFLICT 512 512

FT CONFLICT 477 477

FT CONFLICT 492 492

FT CONFLICT 565 565

SQ SEQUENCE 594 AA: 66896 MM: 9473352 CRC32:

Query Match 70.4%: Score 112: DB 1: Length 594:

Best Local Similarity 70.0%: Pred. No. 7,41e-10:

Matches 14: Conservative 3: Mismatches 3: Indels 0: Gaps 0:

Db 255 SNMSIMARKYKPEVYK 274

Qy 1 SNMYAMMIARFKMPEVYK 20

RESULT 9

ID DCE1\_PIG STANDARD: PRT: 594 AA.

AC P48319;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)

DE (67 KD GLUTAMIC ACID DECARBOXYLASE).

GN GAD1 OR GAD67.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

RA SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;

"Sequences of two porcine glutamic acid decarboxylases (65- and 67-kDa GAD).";

Gene 152:257-260(1995).

RL Gene 152:257-260(1995).

CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.

CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE + CO(2).

CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).

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DR EMBL: D31849; BAA06636.1; -  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC. 1.  
 DR PFAM: PF00282; Pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 PYRIDOXAL PHOSPHATE; Multiligene family.  
 FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 SO SEQUENCE 594 AA; 66894 MW; 69D6C79C CRC32;

Query Match 70.4%; Score 112; DB 1; Length 594;  
 Best Local Similarity 70.0%; Pred. No. 7.41e-10;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 255 SNMYSIMARARYKPEPVKTK 274  
 ||||:| | | | | | | | | |  
 QY 1 SNMYSIMARARYKPEPVKTK 20

RESULT 10  
 ID DCE\_DROME STANDARD; PRT; 510 AA.  
 AC P20228;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).  
 GN GAD OR GLB.  
 OS Drosophila melanogaster (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 OC [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 90155291.  
 RX JACKSON F.R., NEWBY L.M., KULKARNI S.J.;  
 RA "Drosophila GABAergic systems: sequence and expression of glutamic  
 RT acid decarboxylase";  
 RL J. Neurochem. 54:1068-1078(1990).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).  
 CC -----  
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DR EMBL: X76198; CAAS3791.1; -  
 DR PIR: A30999; A30999.  
 DR PIR: JH0192; JH0192.  
 DR FLYBASE: FBgn0004516; Gad1.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC. 1.  
 DR PFAM: PF00282; Pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 PYRIDOXAL PHOSPHATE.  
 FT BINDING 322 322 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 SO SEQUENCE 510 AA; 57758 MW; 97C7ABF1 CRC32;

Query Match 55.3%; Score 88; DB 1; Length 510;  
 Best Local Similarity 63.2%; Pred. No. 1.07e-04;  
 Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 170 SNLYAFIARHKMPNYKE 188  
 ||:| | | | | | | | | |  
 QY 1 SNMYSIMARARYKPEPVKTK 19

RESULT 11  
 ID MAK\_MOUSE STANDARD; PRT; 622 AA.  
 AC 004859;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-  
 DE ASSOCIATED KINASE) (PROTEIN KINASE RCK).  
 GN MAK OR RCK.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 93366030.  
 RX BLADT F., BIRCHMEIER C.;  
 RA "Characterization and expression analysis of the murine rck gene: a  
 RT protein kinase with a potential function in sensory cells";  
 RL Differentiation 53:115-122(1993).  
 CC -1- FUNCTION: COULD HAVE AN IMPORTANT FUNCTION IN SIGNALING PATHWAYS USED  
 CC IN SPERMATOGENESIS. MAY PARTICIPATE IN SIGNALING PATHWAYS USED  
 CC IN VISUAL AND OLFACTORY SENSORY TRANSDUCTION.  
 CC -1- TISSUE SPECIFICITY: IN PRE- AND POSTMEIOTIC MALE GERM CELLS IN  
 CC TESTIS. IN PHOTORECEPTOR CELLS OF THE RETINA AND IN THE OLFACTORY  
 CC RECEPTOR, AND IN CERTAIN EPITHELIA OF THE RESPIRATORY TRACT  
 CC AND CHOROID PLEXUS (BRAIN).  
 CC -1- DEVELOPMENTAL STAGE: ON DAY 14 OR 17 OF EMBRYONIC DEVELOPMENT.  
 CC -1- SIMILARITY: BELONGS TO THE CDC2/CDC28 SUBFAMILY OF SER/THR  
 CC PROTEIN KINASES. BELONGS TO THE CDC2/CDKX SUBFAMILY.  
 CC -----  
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DR EMBL: X66983; CAA47392.1; -  
 DR PIR: S24241; S24241.  
 DR HSSP: P24941; INO1.  
 DR MGD: MGT:96913; MAK.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP. 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST. 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM. 1.  
 DR PFAM: PF00059; Pkinase; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.  
 FT DOMAIN 4 284 PROTEIN KINASE.  
 FT NP\_BIND 10 18 ATP (BY SIMILARITY).  
 FT BINDING 33 33 ATP (BY SIMILARITY).  
 FT ACT\_SITE 125 125 BY SIMILARITY.  
 FT DOMAIN 309 368 GLU/PRO-RICH.  
 SO SEQUENCE 622 AA; 70050 MW; A3D11D70 CRC32;

Query Match 45.3%; Score 72; DB 1; Length 622;  
 Best Local Similarity 53.3%; Pred. No. 1.36e-01;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 85 NLVQLMKDRKLPPE 99  
 ||:| | | | | | | | | |  
 QY 2 NMYSIMARARYKPEPVKTK 16

RESULT 12  
 ID MAK\_RAT STANDARD; PRT; 622 AA.  
 AC P20793;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-  
 DE ASSOCIATED KINASE).





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Msrch\_bp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 7 21:15:14 2000: MasPar time 6.74 Seconds

Tabular output not generated. 205,845 Million cell updates/sec

Title: &gt;US-08-981-824-2

Description: (1-20) from US08981824.pep

Perfect Score: 159

Sequence: 1 SNMYAMMIARFKMFPEVK 20

Scoring table: PAM 150

Gap 15

Searched: 225878-segs, 69334122 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

sptrembl12

1:sp:archaea 2:sp:bacteria 3:sp:fungi 4:sp:human  
5:sp:invertebrate 6:sp:mammal 7:sp:mhc 8:sp:organelle  
9:sp:phage 10:sp:plant 11:sp:rodent 12:sp:unclassified  
13:sp:vertebrate 14:sp:virus

Statistics: Mean 29.459; Variance 46.484; scale 0.634

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	152	95.6	182	13	09W661	GLUTAMATE DECARBOXYLASE 1.86e-17
2	152	95.6	182	13	09W659	GLUTAMATE DECARBOXYLASE 1.86e-17
3	143	88.9	182	13	09W654	GLUTAMATE DECARBOXYLASE 1.92e-15
4	143	88.9	232	13	09J275	GLUTAMATE DECARBOXYLASE 2.46e-14
5	126	75.2	182	13	09W656	GLUTAMATE DECARBOXYLASE 1.01e-11
6	126	75.2	182	13	09W657	GLUTAMATE DECARBOXYLASE 5.15e-10
7	118	74.2	182	13	09W655	GLUTAMATE DECARBOXYLASE 5.15e-10
8	118	74.2	232	13	09J276	GLUTAMATE DECARBOXYLASE 5.15e-10
9	112	70.4	182	13	09W660	GLUTAMATE DECARBOXYLASE 9.32e-09
10	112	70.4	182	13	09W663	GLUTAMATE DECARBOXYLASE 9.32e-09
11	112	70.4	563	13	09I158	GLUTAMATE DECARBOXYLASE 9.32e-09
12	112	70.4	590	13	09Y158	GLUTAMATE DECARBOXYLASE 9.32e-09
13	112	70.4	593	13	09B685	67KD GLUTAMATE DECARBOXYLASE 9.32e-09
14	107	67.3	182	13	09W658	GLUTAMATE DECARBOXYLASE 1.00e-07
15	91	57.2	478	11	064577	CYSTEINE SULFINIC ACID 1.54e-04
16	91	57.2	493	11	064611	CYSTEINE SULFINIC ACID 1.54e-04
17	88	55.3	370	5	044102	GLUTAMATE DECARBOXYLASE 5.80e-04
18	87	54.7	267	4	09Y602	CYSTEINE SULFINIC ACID 8.97e-04
19	87	54.7	267	4	09Y602	CYSTEINE SULFINIC ACID 8.97e-04
20	87	54.7	493	4	09Y600	CYSTEINE SULFINIC ACID 8.97e-04

RESULT ID	1	PRELIMINARY	PRT	182 AA
AC	09W661			
DT	01-NOV-1999	(TREMBlrel. 12, Created)		
DT	01-NOV-1999	(TREMBlrel. 12, Last sequence update)		
DT	01-NOV-1999	(TREMBlrel. 12, Last annotation update)		
DE	GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).			
GN	GAD65.			
OS	Pseudomys scripta (Slender turtle).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Testudines;			
CC	Cryptodira; Testudinoidae; Emydidae; Trachemys.			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN.			
RX	MEDLINE: 99261650.			
RA	BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D., DROUIN G.,			
RA	PRIDE I.G., DOCHERY K., TRUDEAU V.L.,			
RT	"Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:			
RT	molecular phylogeny and evidence for a new GAD paralog."			
RL	Mol. Biol. Evol. 16:397-404(1999).			
DR	EMBL: AF043272; AAD22718.1; -.			
KW	lysase.			
FT	NON TER			
FT	NON TER			
SO	SEQUENCE	182 AA; 19942 MW; 1699125D CRC32;		

## ALIGNMENTS

RESULT ID	1	PRELIMINARY	PRT	182 AA
AC	09W661			
DT	01-NOV-1999	(TREMBlrel. 12, Created)		
DT	01-NOV-1999	(TREMBlrel. 12, Last sequence update)		
DT	01-NOV-1999	(TREMBlrel. 12, Last annotation update)		
DE	GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).			
GN	GAD65.			
OS	Pseudomys scripta (Slender turtle).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Testudines;			
CC	Cryptodira; Testudinoidae; Emydidae; Trachemys.			
LN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN.			
RX	MEDLINE: 99261650.			
RA	BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D., DROUIN G.,			
RA	PRIDE I.G., DOCHERY K., TRUDEAU V.L.,			
RT	"Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:			
RT	molecular phylogeny and evidence for a new GAD paralog."			
RL	Mol. Biol. Evol. 16:397-404(1999).			
DR	EMBL: AF043272; AAD22718.1; -.			
KW	lysase.			
FT	NON TER			
FT	NON TER			
SO	SEQUENCE	182 AA; 19942 MW; 1699125D CRC32;		

Query Match 95.6%; Score 152; DB 13; Length 182;  
Best Local Similarity 95.0%; Pred. No. 1.86e-17;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB	38	SNMYAMMIARFKMFPEVK 57
QY	1	SNMYAMMIARFKMFPEVK 20

RESULT 2  
AC 09W659 PRELIMINARY: PRT: 182 AA.  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).  
GN GAD65.  
OS Psephenus guttata (zebra finch) (Taeniopygia guttata).

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Passeriformes; Estrilidae; Estrilidae; Taeniopygia.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RT PRIDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
RT molecular phylogeny and evidence for a new GAD paralog.";
RT Mol. Biol. Evol. 16:397-404(1999).
DR EMBL: AF043270; AAD22716.1; -.
KW Lyase.
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 19918 MW; B67E4ADF CRC32;

Query Match 95.6%; Score 152; DB 13; Length 182;
Best Local Similarity 95.0%; Pred. No. 1.86e-17;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 38 SNNYAMLARFKMPEVK 57
1 SNNYAMLARFKMPEVK 20
|||||:|||||

RESULT 3
ID 09W654 PRELIMINARY: PRT: 182 AA.
AC 09W654:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD5.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cyprinidae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RT PRIDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
RT molecular phylogeny and evidence for a new GAD paralog.";
RT Mol. Biol. Evol. 16:397-404(1999).
DR EMBL: AF043265; AAD22711.1; -.
KW Lyase.
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 20097 MW; A4A23079 CRC32;

Query Match 89.9%; Score 143; DB 13; Length 182;
Best Local Similarity 85.0%; Pred. No. 1.92e-15;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 38 SNNYAMLARFKMPEVK 57
1 SNNYAMLARFKMPEVK 20
|||||:|||||

RESULT 4
ID 093275 PRELIMINARY: PRT: 232 AA.
AC 093275:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (FRAGMENT).
GN GAD5.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
```

```
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98295903.
RA MARTIN S.C., HEINRICH G., SANDELL J.H.;
RT "Sequence and expression of glutamic acid decarboxylase isoforms in
RT the developing zebrafish.";
RT J. Comp. Neurol. 396:253-266(1998).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
DR EMBL: AF017265; AAC24326.1; -.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; Pyridoxal-dec; 1.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 26059 MW; FD2B274F CRC32;

Query Match 89.9%; Score 143; DB 13; Length 232;
Best Local Similarity 85.0%; Pred. No. 1.92e-15;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 42 SNNYAMLARFKMPEVK 61
1 SNNYAMLARFKMPEVK 20
|||||:|||||

RESULT 5
ID 09W656 PRELIMINARY: PRT: 182 AA.
AC 09W656:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD5.
OS Coryphaenoides armatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Paracanthopterygii; Gadiformes;
OC Macrouridae; Coryphaenoides.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RT PRIDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
RT molecular phylogeny and evidence for a new GAD paralog.";
RT Mol. Biol. Evol. 16:397-404(1999).
DR EMBL: AF043267; AAD22713.1; -.
KW Lyase.
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 19768 MW; 1225481D CRC32;

Query Match 86.8%; Score 138; DB 13; Length 182;
Best Local Similarity 85.0%; Pred. No. 2.46e-14;
Matches 17; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 38 SNNYAMLARFKMPEVK 57
1 SNNYAMLARFKMPEVK 20
|||||:|||||

RESULT 6
ID 09W657 PRELIMINARY: PRT: 182 AA.
AC 09W657:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 67 (EC 4.1.1.15) (FRAGMENT).
GN GAD5.
OS Coryphaenoides armatus.
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01 Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
02 Cyprinoidae; Cyprinidae; Rasbora; Danio.
03 [1]
04 SEQUENCE FROM N.A.
05 RA MEDLINE: 98295903.
06 RA MARTIN S.C., HEINRICH G., SANDELL J.H.:
07 "Sequence and expression of glutamic acid decarboxylase isoforms in
08 the developing zebrafish."
09 J. Comp. Neurol. 396:253-266(1998).
10 CC -1- CONECTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
11 -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
12 TYRDC).
13 DR EMBL: AF017266; AAC24327.1; -.
14 DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
15 DR PFAM: PF00282; Pyridoxal_dec; 1.
16 KM Lysase; Decarboxylase; Pyridoxal phosphate.
17 FT NON_TER 1
18 FT NON_TER 1
19 FT NON_TER 1
20 SO SEQUENCE 232 AA; 23676 MW; C7DC7A63 CRC32;
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22 Query Match 74.2%; Score 118; DB 13; Length 232;
23 Best Local Similarity 70.0%; Pred. No. 5,15e-10;
24 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0.
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26 Db 42 SNMYSVMARKYPEVVKTK 61
27 QY 1 SNMYSVMARKYPEVVKTK 20
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;  
 OC Cryptodira; Testudinoidea; Emydidae; Trachemys.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 99261650.  
 RA BOSMA P.T., BLAQUERE M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,  
 PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;  
 RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:  
 molecular phylogeny and evidence for a new GAD paralog."  
 RL Mol. Biol. Evol. 16:397-404(1999).  
 DR EMBL: AF043274; AAD22720.1;  
 KW Lyase.  
 FT NON\_TER  
 SQ SEQUENCE 182 AA; 20047 MW; 002023C1 CRC32;  
 Query Match 70.4%; Score 112; DB 13; Length 182;  
 Best Local Similarity 70.0%; Pred. No. 9.32e-09;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 38 SNMYSIMARKYKPEVKTK 57  
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 QY 1 SNMYSIMARKYKPEVKTK 20

RESULT 11  
 ID 091644 PRELIMINARY; PRT; 563 AA.  
 AC 091644;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE GLUTAMIC ACID DECARBOXYLASE.  
 GN GAD.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;  
 OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;  
 OC Xenopus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA WART S.D., SPITZER N.C.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY)  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 DR EMBL: U38225; AAA96273.1;  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; Pyridoxal dec. 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 563 AA; 64095 MW; CBBB0C98 CRC32;

Query Match 70.4%; Score 112; DB 13; Length 563;  
 Best Local Similarity 70.0%; Pred. No. 9.32e-09;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 224 SNMYSIMARKYKPEVKTK 243  
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 QY 1 SNMYSIMARKYKPEVKTK 20

RESULT 12  
 ID 09158 PRELIMINARY; PRT; 590 AA.  
 AC 09158;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE 67.  
 GN GAD67.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;  
 CC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-WHITE LECHORN;  
 RA WAGBERG F.;  
 RT "Characterization of glutamate decarboxylase in chicken."  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 DR EMBL: AF030355; AAD01902.1;  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 590 AA; 66710 MW; 80B66DFE CRC32;  
 Query Match 70.4%; Score 112; DB 13; Length 590;  
 Best Local Similarity 70.0%; Pred. No. 9.32e-09;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 251 SNMYSIMARKYKPEVKTK 270  
 ||||:|||||  
 QY 1 SNMYSIMARKYKPEVKTK 20

RESULT 13  
 ID 008685 PRELIMINARY; PRT; 593 AA.  
 AC 008685;  
 DT 01-JUL-1997 (TREMBlrel. 04, Created)  
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE 67KD GLUTAMIC ACID DECARBOXYLASE.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RA AUST G., STEINBRENNER H., THAMM B., ROST A.K., SEISSLER J.;  
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 DR EMBL: Y12257; CAA72934.1;  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; Pyridoxal dec. 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 593 AA; 66648 MW; BAF92E0 CRC32;

Query Match 70.4%; Score 112; DB 11; Length 593;  
 Best Local Similarity 70.0%; Pred. No. 9.32e-09;  
 Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Db 254 SNMYSIMARKYKPEVKTK 273  
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 QY 1 SNMYSIMARKYKPEVKTK 20

RESULT 14  
 ID 09W658 PRELIMINARY; PRT; 182 AA.  
 AC 09W658;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE ISOFORM 3 (EC 4.1.1.15) (FRAGMENT).  
 GN GAD3.  
 OS Coryphaenoides armatus.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;  
 OC Neopterygii; Teleostei; Euteleostei; Paracanthopterygii; Gadiformes;  
 OC Macrouridae; Coryphaenoides.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 99261650.  
 RA BOSMA P.T., BLAQUERE M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,  
 PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;  
 RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:"



PT Molecular phylogeny and evidence for a new GAD paralog.  
 cl. MOI. Biol. Evol. 16:397-404(1999).  
 DR EMBL: AF043269; AAD2715.1; -.  
 KW Lyase.  
 FT NON\_TER 1 1  
 FT NON\_TER 182 182  
 SQ SEQUENCE 182 AA; 19812 MW; 30183853 CRC32;

Query Match 67.3%; Score 107; DB 13; Length 182;  
 Best Local Similarity 50.0%; Pred. No. 1.00e-07;  
 Matches 10; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Db 38 SNLYSMIVARYALYPPDVKTK 57  
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 Qy 1 SNMYAMMIARFKMPPEVK 20

RESULT 15  
 ID 064577 PRELIMINARY: PRT: 478 AA.  
 AC 064577;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-NOV-1999 (TRENBLREL. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)  
 DE (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).  
 OS Rattus norvegicus (rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY;  
 RX MEDLINE: 95290499.  
 RA KATSUKIA P.J., JERKINS A.A., GOODSPEED D.C., STEELE R.D.;  
 RT "Cloning and characterization of rat cysteine sulfinic acid  
 decarboxylase."  
 RL Biochim. Biophys. Acta 1262:79-82(1995).  
 CC -1- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE = HYPOTAURINE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).  
 DR EMBL: M64755; AAC42063.1; -.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PRAM: PF00282; pyridoxal\_dec; 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 478 AA; 53725 MW; 4CAC0093 CRC32;

Query Match 57.2%; Score 91; DB 11; Length 478;  
 Best Local Similarity 50.0%; Pred. No. 1.54e-04;  
 Matches 10; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 155 SNMYAINLARFORYPDCKOR 174  
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 Qy 1 SNMYAMMIARFKMPPEVK 20

Search completed: Tue Mar 7 21:15:23 2000  
 Job time : 9 secs.

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Mpsrch\_dp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Mar 7 21:26:23 2000; Maspar time 3.91 Seconds  
 Tabular output not generated. 121.227 Million cell updates/sec

Title: >US-08-981-824-3  
 Description: (1-20) from US08981824.pep  
 Perfect Score: 154  
 Sequence: 1 NWEIADQPONLEIIMHCOT 20

Scoring table: PAM 150  
 Gap 15

Searched: 188965 segs, 23686106 residues  
 Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: a-geneseq35  
 1:geneseqp

Statistics: Mean 21.001; Variance 73.034; scale 0.288

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	154	100.0	20	1	W01795 Human 65 kD glutamine	1.92e-08
2	154	100.0	20	1	W18844 65 kD glutamic acid de	1.92e-08
3	154	100.0	503	1	R23645 Human GAD65 gene produ	1.92e-08
4	154	100.0	540	1	R59520 GAD65 1-45 N-terminal-	1.92e-08
5	154	100.0	544	1	R59524 GAD65 545-585 C-termi	1.92e-08
6	154	100.0	554	1	R59518 GAD65 1-31 deleted, C4	1.92e-08
7	154	100.0	584	1	R56017 Human GAD65 protein se	1.92e-08
8	154	100.0	584	1	W34519 Human GAD65 protein	1.92e-08
9	154	100.0	585	1	W12402 65 kD human glutamic a	1.92e-08
10	154	100.0	585	1	W14915 Modified glutamic acid	1.92e-08
11	154	100.0	585	1	R28756 Human pancreatic islet	1.92e-08
12	154	100.0	585	1	R59516 Human GAD65	1.92e-08
13	154	100.0	585	1	R79105 Human glutamic acid de	1.92e-08
14	154	100.0	585	1	W14916 Modified glutamic acid	1.92e-08
15	154	100.0	585	1	R29629 Human GAD 65	1.92e-08
16	154	100.0	585	1	R29629 Human GAD 65	1.92e-08
17	154	100.0	585	1	W35361 Human 65K-glutamic aci	1.92e-08
18	142	92.2	540	1	R59521 GAD65 1-45 N-terminal-	4.06e-07
19	142	92.2	544	1	R59525 GAD65 545-585 C-termi	4.06e-07
20	142	92.2	554	1	R59519 GAD65 1-31 deleted, C4	4.06e-07
21	142	92.2	584	1	W86018 Rat GAD65 protein sequ	4.06e-07
22	142	92.2	584	1	W34520 Rat GAD65 protein	4.06e-07
23	142	92.2	585	1	R23644 Rat GAD65 gene product	4.06e-07

\*\*\*\*\*  
 W01795-1997 (first entry)  
 DE Human-65 kD glutamine decarboxylase peptide.  
 KW Human; glutamine decarboxylase; GAD; diagnosis; predisposition;  
 KW tumour; immunological; disease; autoimmune; diabetes; reagent;  
 KW determination; T cell; subpopulation; medicament; treatment;  
 KW prevention; production; antigen; immunogen; tolerogen; isolation;  
 KW reinjection; inactivation.  
 OS Homo sapiens.  
 PN DE19525784-A1.  
 PD 16-JAN-1997.  
 PF 14-JUL-1995; 025784.  
 PR 14-JUL-1995; DE-025784.  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH  
 PI Albert W, Boltard C, Endl J, Jung G, Schendel D;  
 PI Stahl P, Van Ender P;  
 DR WPI: 97-078452/08.  
 PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of  
 PT diabetes, etc.  
 PS Claim 1; Page 12; 15pp; German.  
 CC The present peptide is a fragment of the human 65 kD glutamine  
 CC decarboxylase (GAD), which can be used to diagnose, or diagnose a  
 CC predisposition to, a tumour or immunological disease, preferably an  
 CC autoimmune disease, especially diabetes. It can also be used as a  
 CC reagent to determine specific T cell subpopulations, in medicaments  
 CC to treat or prevent immunological diseases, preferably autoimmune  
 CC diseases, especially diabetes, to produce antigens, especially  
 CC immunogens or tolerogens and to isolate specific T cell  
 CC subpopulations, which can be used to produce antigens or for  
 CC reinjection, optionally after inactivation.  
 SQ Sequence 20 AA:  
 Query Match 100.0%; Score 154; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 NWEIADQPONLEIIMHCOT 20  
 QY 1 NWEIADQPONLEIIMHCOT 20  
 RESULT 2  
 ID W18844 standard; peptide; 20 AA.  
 AC W18844;  
 DT 05-JAN-1998 (first entry)

24 142 92.2 585 1 R29628 Rat GAD 65. 4.06e-07  
 25 142 92.2 585 1 R59517 Rat GAD65. 4.06e-07  
 26 142 92.2 605 1 R71733 Rat glutamic acid deca 4.06e-07  
 27 120 77.9 22 1 R72270 Glutamic acid decarbox 9.95e-05  
 28 85 55.8 593 1 R27220 Brain GAD #2. 3.49e-01  
 29 86 55.8 594 1 R27222 Full length islet GAD. 3.49e-01  
 30 86 55.8 594 1 W74717 Amino acid sequence of 3.49e-01  
 31 86 55.8 594 1 R27221 Full length brain GAD. 3.49e-01  
 32 86 55.8 594 1 W74716 Amino acid sequence of 3.49e-01  
 33 82 53.2 368 1 W99093 Rhodospiridium torula 8.76e-01  
 34 82 53.2 368 1 W31362 R. gracilis D-amino ac 8.76e-01  
 35 72 45.8 20 1 R72271 Glutamic acid decarbox 8.35e+00  
 36 63 40.9 429 1 R10976 Polyhydroxyalkanoate p 5.30e+01  
 37 61 39.6 483 1 W31338 Amino acid sequence of 9.01e+01  
 38 60 39.0 663 1 W09055 Nicotiana glauca plumb 1.11e+02  
 39 60 39.0 666 1 R75366 Adhesin. 1.11e+02  
 40 58 37.7 152 1 Y07969 Human secreted protein 1.68e+02  
 41 58 37.7 357 1 W85465 Secreted protein encod 1.68e+02  
 42 58 37.7 748 1 W03174 Mouse STAT3. 1.68e+02  
 43 58 37.7 748 1 R72081 Mouse Stat4 (13stl). 1.68e+02  
 44 58 37.7 3587 1 R34713 Bacillus subtilis srfA 1.68e+02  
 45 58 37.7 3588 1 R34712 Bacillus subtilis srfA 1.68e+02

DE 65 kD glutamic acid decarboxylase peptide fragment III  
KW GAD: 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;  
KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;  
KW predilection: autoimmune; tumour; rheumatoid arthritis;  
KW multiple sclerosis  
OS Synthetic.  
PN DE19526561-A1.  
PD 23-JUN-1997.  
PF 20-JUL-1995; DE-026561.  
PR (BOER) BOEHRINGER MANNHEIM GMBH.  
PA Dönitz F, Endl J, Ganz M, Jung G, Kientsch-Engel R;  
PI Pozzilli P, Stahl P;  
DR WPI: 97-088254/09.  
PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -  
involving intradermal admin. of auto-reactive substances  
PS Claim 11: Page 9; 12pp; German.  
CC M18842-70 are peptide fragments of the 65 kD human glutamic acid  
decarboxylase (GAD). The fragments are autoreactive substances used for  
diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is  
determined by using a claimed method for diagnosis of cell-mediated  
diseases or a predilection to cell-mediated diseases, which is effected  
by administering an autoreactive substance intradermally and establishing  
the diagnosis on the basis of the occurrence or lack of a positive  
reaction at the site of administration. The method is used for diagnosis  
of autoimmune and tumour diseases, preferably T-cell-mediated diseases  
such as rheumatoid arthritis, multiple sclerosis and especially IDDM.  
SQ Sequence 20 AA;

Query Match 100.0%; Score 154; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1,92e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dd 1 NMELADQPONLEIIMHCOT 20  
|||  
QY 1 NMELADQPONLEIIMHCOT 20

RESULT 3  
ID R23645 standard; Protein: 503 AA.  
AC R23645;  
DT 02-NOV-1992 (first entry)  
DE Human GAD65 gene product.  
KW Glutamic acid decarboxylase; IDDM; stiff man syndrome;  
KW autoantibodies.  
OS Homo sapiens.  
PN WO9205446-A.  
PD 02-APR-1992.  
PF 23-SEP-1991; 006872.  
PR 21-SEP-1990; US-386536.  
PA (REGC) UNIV CALIFORNIA.  
PA (REGC) UNIV CALIFORNIA.  
PA (REGC) UNIV OF CALIFORNIA.  
PI Erlanger MG, Kaufman DL, Tobin AJ;  
DR WPI: 92-150489/18.  
DR N-PSDB: Q24184.  
PT Novel cDNA encoding GAD65 polypeptide - used to produce GAD65 for  
therapeutic and diagnostic application in insulin-dependent  
PT diabetes mellitus patients  
PS Disclosure: Fig 3: 53pp; English.  
CC The sequence given is a glutamic acid decarboxylase (GAD65). GAD65  
can be used for the diagnosis and therapy of patients with autoimmune  
diseases, esp. insulin-dependent diabetes mellitus (IDDM) and "stiff  
CC man" syndrome. It is possible to use either the entire GAD65 protein  
or polypeptide fragments of it for the immunological detection of  
CC autoantibodies to GAD65 which are indicative of IDDM and other auto-  
immune diseases. The production of this sequence by recombinant DNA  
CC technology allows large scale production of eukaryotic GAD65 in its  
CC native form without the need for separation from other proteinaceous  
CC prods.  
SQ Sequence 503 AA;

Query Match 100.0%; Score 154; DB 1; Length 503;

Best Local Similarity 100.0%; Pred. No. 1,92e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Dd 146 NMELADQPONLEIIMHCOT 165  
|||  
QY 1 NMELADQPONLEIIMHCOT 20

RESULT 4  
ID R59520 standard; Protein: 540 AA.  
AC R59520;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-45 N-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Narnhofer M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 540 AA;

Query Match 100.0%; Score 154; DB 1; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1,92e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dd 101 NMELADQPONLEIIMHCOT 120  
|||  
QY 1 NMELADQPONLEIIMHCOT 20

RESULT 5  
ID R59524 standard; Protein: 544 AA.  
AC R59524;  
DT 09-NOV-1994 (first entry)  
DE GAD65 545-585 C-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Narnhofer M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. The C-terminally deleted mutants given in R59524-25  
CC are able to recognize IDDM autoantibodies having the specificity  
CC of MICA4/MICA6, but not those having the specificity of MICA1/MICA3  
CC or MICA2. These mutants also have some N-terminal modifications  
CC to improve solubility.  
SQ Sequence 544 AA;

Query Match 100.0%; Score 154; DB 1; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADOPONLEILMHCOT 165  
 ||||||||||||||||  
 QY 1 NWELADOPONLEILMHCOT 20

RESULT 6  
 ID R59518 standard; protein: 554 AA.  
 AC R59518;  
 DT 09-NOV-1994 (first entry)  
 DE GAD65 1-31 deleted; C45A mutant.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 OS Homo sapiens.  
 PN M09412539-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (RECC) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure: Fig. 1: 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 554 AA;

Query Match 100.0%; Score 154; DB 1; Length 554;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 115 NWELADOPONLEILMHCOT 134  
 ||||||||||||||||  
 QY 1 NWELADOPONLEILMHCOT 20

RESULT 7  
 ID W86017 standard; protein: 584 AA.  
 AC W86017;  
 DT 22-FEB-1999 (first entry)  
 DE Human GAD65 protein sequence.  
 KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
 KW insulin-dependent diabetes mellitus; stiff man syndrome.  
 OS Homo sapiens.  
 PN US5849506-A.  
 PD 15-DEC-1998.  
 PF 25-MAY-1993; 450755.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PR 25-MAY-1995; US-450755.  
 PA (RECC) UNIV CALIFORNIA.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 99-069120/06.  
 PT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
 PT diabetes and stiff man syndrome  
 PS Examples: Fig 1: 31pp; English.  
 CC This represents a human GAD65 protein sequence. The invention provides  
 CC soluble fragments of GAD65 that are specifically reactive with at least  
 CC one class of GAD65 autoantibody. The fragments are substantially free of  
 CC N-terminal amino acids that would otherwise limit solubility. Different  
 CC fragments contain different epitopes for different classes of GAD65  
 CC autoantibodies. These fragments are used in the methods of the invention  
 CC for detection of GAD65 autoantibodies. The methods are used for  
 CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and

CC stiff man syndrome.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 154; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADOPONLEILMHCOT 165  
 ||||||||||||||||  
 QY 1 NWELADOPONLEILMHCOT 20

RESULT 8  
 ID W34519 standard; protein: 584 AA.  
 AC W34519;  
 DT 24-MAR-1998 (first entry)  
 DE Human GAD65 protein.  
 KW GAD65; glutamic acid decarboxylase protein; human; soluble fragment;  
 KW autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
 KW stiff man syndrome; therapy.  
 OS Homo sapiens.  
 PN US5691448-A.  
 PD 25-NOV-1997.  
 PF 02-DEC-1993; 161290.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PA (BAEK/) BAEKESKOV S.  
 PA (KIM/) KIM J.  
 PA (NAMC/) NAMCHUK M.  
 PA (RICH/) RICHTER W.  
 PA (SHI/) SHI Y.  
 PI Baekkeskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 98-017711/02.  
 PT Soluble fragments of glutamic acid decarboxylase GAD65 - used to  
 PT distinguish between insulin-dependent diabetes mellitus and  
 PT stiff-man syndrome  
 PS Disclosure: column 27-30, 30pp; English.  
 CC This sequence represents the human glutamic acid decarboxylase protein  
 CC GAD65. The invention relates to soluble fragments of a GAD65 protein that  
 CC are specifically reactive with a GAD65 autoantibody (AAb), where the  
 CC fragment is at least 99% pure and the AAb binds to a conformational  
 CC epitope of the fragment. The soluble GAD65 fragments can be used to  
 CC distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff  
 CC man syndrome. They can also be used for diagnosis and treatment of IDDM  
 CC and stiff man syndrome. The fragments can distinguish different temporal  
 CC stages in the progression of IDDM.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 154; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADOPONLEILMHCOT 165  
 ||||||||||||||||  
 QY 1 NWELADOPONLEILMHCOT 20

RESULT 9  
 ID W12402 standard; protein: 585 AA.  
 AC W12402;  
 DT 08-OCT-1997 (first entry)  
 DE 65 kD human glutamic acid decarboxylase isoform.  
 KW 65 kD glutamic acid decarboxylase; human; GAD65; enzyme; pancreas;  
 KW neuron; central nervous system; type I diabetes; autoimmune response;  
 KW T cell; therapy.  
 OS Homo sapiens.  
 PN W09700891-A1.  
 PD 09-JAN-1997.  
 PF 24-JUN-1996; U10790.  
 PR 23-JUN-1995; US-494624.  
 PA (KENN-) KENNEDY INST RHEUMATOLOGY.  
 PA (NEUR-) NEUROCRINE BIOSCIENCES, INC.  
 PA (SBAR-) ST BARTHOLOMEW S HOSPITAL CENT CLINICAL.

PI Conlon PJ, Gaur A, Leslie RDG, Ling N, Longei M;  
 DR WPI: 97-087322/08.  
 DR N-PSDB: T61097.  
 PT New human glutamic acid decarboxylase peptide(s) - used for  
 PT treatment, diagnosis and determining predisposition to diabetes and  
 PT for ameliorating auto-immune responses.  
 PS Disclosure: Fig 1: 28pp; English.  
 CC This sequence represents the 65 kD isoform of human glutamic acid  
 CC decarboxylase (GAD65). GAD is an enzyme expressed in the beta cells of  
 CC the pancreas, and in neurons of the central nervous system. There are two  
 CC isoforms of GAD, a 67 kD isoform, and GAD65. Immunodominant regions of  
 CC GAD65 have been identified in Type I diabetic patients. Fragments of  
 CC GAD65, and analogues of the fragments, are used in the methods of the  
 CC invention. The methods are for detecting or treating diabetes or a  
 CC predisposition to diabetes. The peptides can also be used for  
 CC ameliorating an autoimmune response in a patient. Alteration of the  
 CC native peptides with selective changes of crucial residues can induce  
 CC unresponsiveness or change the responsiveness of antigen-specific  
 CC autoreactive T cells. The peptide analogues compete for binding to MHC  
 CC and do not cause proliferation of the corresponding native  
 CC peptide-specific T cells.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWEIADQPONEEILMHCO 165  
 OY 1 NWEIADQPONEEILMHCO 20

RESULT 10  
 ID W14915 standard; Protein; 585 AA.  
 AC W14915;  
 DT 10-JUL-1997 (first entry)  
 DE Modified glutamic acid decarboxylase (K396R).  
 KW Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;  
 KW Insulin-dependent diabetes mellitus; vaccine;  
 KW enzyme engineering; protein engineering.  
 OS Synthetic.  
 PN WO9712034-A1.  
 PD 03-APR-1997.  
 PF 27-SEP-1996; SE1210.  
 PR 26-SEP-1995; SE-003379.  
 PA (SYNE-) SYNECTICS BIOTECHNOLOGY AB.  
 PI Essen-Moeller A, Falorni A, Lernmark A, Robertson J;  
 DR WPI: 97-212895/19.  
 DR N-PSDB: T64560.  
 PT Modified glutamic acid decarboxylase for autoimmune disease  
 PT treatment - has immunoreactivity of unmodified GAD65 but decreased  
 PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus  
 PT treatment  
 PS Claim 3: Page 13-15; 24pp; English.  
 CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the  
 CC native lysine residue at amino acid position 386 replaced by  
 CC arginine. It is obcd. by site-directed mutagenesis (see also  
 CC T64561) of native human GAD65 cDNA and expression of the mutant DNA  
 CC (T64560) in transformed host cells. Lys-386 is critical for enzyme  
 CC activity. By replacing it with an amino acid incapable of Schiff  
 CC base formation, immunoreactivity is maintained but enzyme activity  
 CC is reduced or lost, so minimizing the risk of toxicity. The  
 CC modified GAD can be used to treat and/or prevent autoimmune  
 CC disorders such as insulin-dependent diabetes mellitus (IDDM) and  
 CC other diseases, e.g. neurological diseases, esp. in individuals  
 CC having a genetic predisposition for IDDM or with an increased  
 CC antibody titre against GAD.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWEIADQPONEEILMHCO 165  
 OY 1 NWEIADQPONEEILMHCO 20

RESULT 11  
 ID R28756 standard; Protein; 585 AA.  
 AC R28756;  
 DT 20-APR-1993 (first entry)  
 DE Human pancreatic islet cell glutamic acid decarboxylase.  
 KW GAD; insulin dependent diabetes mellitus; IDDM; autoantibody detection.  
 OS Homo sapiens.  
 PN WO9220811-A.  
 PD 26-NOV-1992.  
 PF 14-MAY-1992; U04079.  
 PR 15-MAY-1991; US-702162.  
 PA (UNIW ) UNIV WASHINGTON.  
 PI (ZYMO ) ZYMOGENETICS INC.  
 PT Foster DC, Grubin CE, Hagopian W, Karlson AE, Lernmark A, Ohara PJ;  
 DR WPI: 92-415789/50.  
 DR N-PSDB: Q31783.  
 PT Polynucleotide encoding human islet glutamic acid decarboxylase -  
 PT used to test for auto-antibodies against itself to diagnose  
 PT insulin dependent diabetes mellitus  
 PS Disclosure: Fig 2: 45pp; English.  
 CC The sequence is that of human pancreatic islet glutamic acid  
 CC decarboxylase (GAD) which is used to test biological samples for  
 CC the presence of autoantibodies to human GAD. It can also be used  
 CC to remove antibodies against GAD from plasma in order to treat an  
 CC autoimmune response to GAD, e.g. in insulin-dependent diabetes mellitus  
 CC (IDDM), and may also be used to induce immunological tolerance to GAD  
 CC by giving GAD that specifically binds the GAD receptor on immature T  
 CC or B cells.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWEIADQPONEEILMHCO 165  
 OY 1 NWEIADQPONEEILMHCO 20

RESULT 12  
 ID R59516 standard; Protein; 585 AA.  
 AC R59516;  
 DT 09-NOV-1994 (first entry)  
 DE Human GAD65.  
 KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
 KW stiff man syndrome; autoantibody.  
 OS Homo sapiens.  
 PN WO9412529-A.  
 PD 09-JUN-1994.  
 PF 02-DEC-1993; U11705.  
 PR 03-DEC-1992; US-984935.  
 PA (RBGC ) UNIV CALIFORNIA.  
 PI Baekskov S, Kim J, Nanchuk M, Richter W, Shi Y;  
 DR WPI: 94-200193/24.  
 PT New soluble fragments of glutamic acid decarboxylase protein -  
 PT used for the diagnosis and treatment of insulin dependent  
 PT diabetes mellitus and stiff man syndrome.  
 PS Disclosure: Fig. 1: 73pp; English.  
 CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
 CC (R59517) were determined. New soluble fragments of GAD65  
 CC (R59518-25) were prepared by deletion/substitution  
 CC mutagenesis. These fragments are free of N-terminal amino acids  
 CC that limit solubility. Different fragments contain epitopes for  
 CC different classes of GAD65 autoantibodies.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;

Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEIIMHCQT 165  
 |||||||  
 QY 1 NWELADQPONLEIIMHCQT 20

RESULT 13  
 ID R79105 standard; Protein: 585 AA.  
 AC R79105;  
 DT 13-NOV-1995 (first entry)  
 DE Human glutamic acid decarboxylase (GAD65).  
 KW Rat glutamic acid decarboxylase; GAD65; autoimmune disorders;  
 KM Insulin-dependent diabetes mellitus; stiff man disease.  
 OS Homo sapiens.  
 PN WO9507992-A.  
 PD 23-MAR-1995.  
 PF 24-AUG-1994; U09478.  
 PR 17-SEP-1993; US-123859.  
 PA (RECC ) UNIV CALIFORNIA.  
 PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;  
 DR MPI: 95-131360/17.  
 N-PSDB: Q86482.  
 PT New polypeptide fragments of glutamic acid decarboxylase - for  
 PT diagnosis and treatment of autoimmune disease, esp. insulin  
 PT dependent diabetes; also related nucleic acid, vectors,  
 PT antibodies, hydridoma(s) etc.  
 CC Example 1: Fig 3; 100bp; English.  
 CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic  
 CC acid decarboxylase (GAD65) respectively, from which the GAD65  
 CC fragments described in R72261-R72298 were derived. These fragments  
 CC can be used to detect autoantibodies against GAD, e.g. to diagnose  
 CC and treat GAD-related autoimmune disorders, such as insulin  
 CC dependent diabetes mellitus or stiff man disease.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEIIMHCQT 165  
 |||||||  
 QY 1 NWELADQPONLEIIMHCQT 20

RESULT 14  
 ID W14916 standard; Protein: 585 AA.  
 AC W14916;  
 DT 10-JUL-1997 (first entry)  
 DE Modified glutamic acid decarboxylase.  
 KW Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;  
 KM Insulin-dependent diabetes mellitus; vaccine;  
 OS Synthetic.  
 FH Key Location/Qualifiers  
 FT msc\_difference 396  
 FT /label= Ile, Arg, Gln, His, Gly  
 PN WO9712034-A1.  
 PD 03-APR-1997.  
 PF 27-SEP-1996; SFL1210.  
 PR 29-SEP-1995; SE-003379.  
 PA (SYNE-) SYNECTICS BIOTECHNOLOGY AB.  
 PI Essen-Moeller A, Falorni A, Lernmark A, Robertson J;  
 DR MPI: 97-212895/19.  
 PT Modified glutamic acid decarboxylase for autoimmune disease  
 PT treatment - has immunoreactivity of unmodified GADs but decreased  
 PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus  
 PT treatment  
 PS Claim 1: Page 16-18; 24pp; English.  
 CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the  
 CC native Lys residue at amino acid position 396 replaced by Ile, Gln,  
 CC His, Gly or esp. Arg (see also W14915). It is obt. by site-  
 CC directed mutagenesis of native human GAD65 cDNA and expression of

CC the mutant DNA in transformed host cells. Lys-396 is critical for  
 CC enzyme activity. By replacing it with an amino acid incapable of  
 CC Schiff base formation, immunoreactivity is maintained but enzyme  
 CC activity is reduced or lost, so minimizing the risk of toxicity.  
 CC The modified GAD can be used to treat and/or prevent autoimmune  
 CC disorders such as insulin-dependent diabetes mellitus (IDDM) and  
 CC other diseases, e.g. neurological diseases, esp. in individuals  
 CC having a genetic predisposition for IDDM or with an increased  
 CC antibody titre against GAD.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEIIMHCQT 165  
 |||||||  
 QY 1 NWELADQPONLEIIMHCQT 20

RESULT 15  
 ID R71641 standard; Protein: 585 AA.  
 AC R71641;  
 DT 21-SEP-1995 (first entry)  
 DE Human GAD.  
 KW GAD; glutamic-acid-decarboxylase; glutamate-decarboxylase;  
 KM non-insulin-dependent diabetes; NIDDM; diagnosis; autoantibody;  
 KW pancreas; islet.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT binding-site 394..399  
 FT /label= Pyridoxal-5'-phosphate-binding-site  
 PN WO9507464-A.  
 PD 16-MAR-1995.  
 PF 02-SEP-1994; U09937.  
 PR 07-SEP-1993; US-117907.  
 PA (UNITV ) UNIV WASHINGTON.  
 PI Hagopian W, Karlens AE, Landin-Olsson M, Lernmark A;  
 DR MPI: 95-123512/16.  
 N-PSDB: Q86046.  
 PT Predicting the clinical course of diabetes in patients with  
 PT non-insulin dependent diabetes mellitus - by detecting the  
 PT presence of autoantibodies to human islet cell glutamic acid  
 PT decarboxylase.  
 PS Claim 8: Page 40-44; 62pp; English.  
 CC A human islet cDNA library was screened for colonies containing  
 CC GAD cDNA using probes (given in Q86047-49) based on conserved  
 CC internal and N- and C-terminal regions of cat, rat and mouse brain  
 CC GAD. Full-length clones were obtained by PCR-RACE. The entire  
 CC sequence of the human islet GAD cDNA is given in Q86046 and the  
 CC encoded protein in R71641. GAD was used to screen sera for the  
 CC presence of GAD autoantibodies.  
 SQ Sequence 585 AA;

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.92e-08;  
 Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 146 NWELADQPONLEIIMHCQT 165  
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 QY 1 NWELADQPONLEIIMHCQT 20

Search completed: Tue Mar 7 21:26:31 2000  
 Job time : 8 secs.

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Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,
A.J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
#cross-references MUID:92196068
#accession A41935
##molecule_type mRNA
##residues 1-585 ##label BUI
##cross-references GB:M81882; NID:q182933; PIDN:AAA62367.1; PID:q182934
#experimental_source brain
#note sequence extracted from NCBI backbone (NCBIP:88007)
REFERENCE
#authors A41292
Karlsten, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
Disteche, C.M.; Adler, D.A.; Baetmeier, H.; Mathewes, S.;
Grant, F.J.; Foster, D.; Lermarck, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
#title Cloning and primary structure of a human islet isoform of
glutamic acid decarboxylase from chromosome 10.
#cross-references MUID:92020848
#accession A41292
##molecule_type mRNA
##residues 1-585 ##label KAR
##cross-references GB:M74826; NID:q182931; PIDN:AAA58491.1; PID:q182932
#experimental_source pancreatic islet
REFERENCE
#authors Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel,
B.; Northemann, W.
#journal Eur. J. Biochem. (1993) 212:597-603
#title Characterization of a linear epitope within the human
pancreatic 64-kDa glutamic acid decarboxylase and its
autoimmune recognition by sera from insulin-dependent
diabetes mellitus patients.
#cross-references MUID:93185681
#accession S30058
##molecule_type mRNA
##residues 6-585 ##label MAU
##cross-references EMBL:X69936
#experimental_source pancreatic islet
REFERENCE
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2)
encoding two human glutamate decarboxylases (GAD-67 and
GAD-65) suggests that they derive from a common ancestral
GAD.
#cross-references MUID:94375018
#contents annotation: intron-exon boundaries
#comment This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene. GAD has
also been implicated as an autoantigen in autoimmune disease
stiff-man syndrome and insulin-dependent diabetes mellitus.
GENETICS
#gene GDB:GAD2
##cross-references GDB:128595; OMIM:138275
#map_position 10p11.23-10p11.23
CLASSIFICATION
#superfamily human glutamate decarboxylase
KEYWORDS
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
396 #binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
SUMMARY
#length 585 #molecular_weight 65411 #checksum 4799
Query Match 100.0%; Score 154; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 5,286-19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 146 NWELADOPONLEILHCOT 165
|||||
OY 1 NWELADOPONLEILHCOT 20
|||||

Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,
A.J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
#cross-references MUID:92196068
#accession A41935
##molecule_type mRNA
##residues 1-585 ##label BUI
##cross-references GB:M81882; NID:q182933; PIDN:AAA62367.1; PID:q182934
#experimental_source brain
#note sequence extracted from NCBI backbone (NCBIP:88007)
REFERENCE
#authors A41292
Karlsten, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
Disteche, C.M.; Adler, D.A.; Baetmeier, H.; Mathewes, S.;
Grant, F.J.; Foster, D.; Lermarck, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
#title Cloning and primary structure of a human islet isoform of
glutamic acid decarboxylase from chromosome 10.
#cross-references MUID:92020848
#accession A41292
##molecule_type mRNA
##residues 1-585 ##label ERL
##cross-references GB:M72422; NID:q204225; PIDN:AAA63488.1; PID:q204226
#experimental_source brain
#note The authors translated the codon GAT for residue 86 as
His, TCA for residue 198 as Ala, and CAG for residue
428 as Trp
REFERENCE
#authors Chang, Y.C.; Gottlieb, D.I.
#journal J. Neurosci. (1988) 8:2123-2130
#title Characterization of the proteins purified with monoclonal
antibodies to glutamic acid decarboxylase.
#cross-references MUID:88258610
#accession A60888
##status preliminary
##molecule_type protein
##residues 'V',191-194,'X',195-203,'XX',206-219,'X',225-234,'X',
'X',236-247,'X',249-266,'X',524-537,539-543,'V',547-549,
'X',551-553,'X',555-558 ##label CHA
#comment This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene.
CLASSIFICATION
#superfamily human glutamate decarboxylase
KEYWORDS
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
396 #binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
SUMMARY
#length 585 #molecular_weight 65402 #checksum 7756
Query Match 92.2%; Score 142; DB 1; Length 585;
Best Local Similarity 95.0%; Pred. No. 3,276-16;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 146 NWELADOPONLEILHCOT 165
|||||
OY 1 NWELADOPONLEILHCOT 20
|||||

Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.
#journal Biochim. Biophys. Acta (1993) 1216:157-160
#title Cloning and sequence analysis of a murine cDNA encoding
glutamate decarboxylase (GAD65).
#cross-references MUID:94032481
#accession S38533
##status preliminary
##molecule_type mRNA
##residues 1-585 ##label LEE

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##cross-references GB:LI6980; NID:g413867; PIDN:AAA93049.1; PID:g413868  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal  
phosphate  
FEATURE  
396 #binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 585 #molecular-weight 65224 #checksum 7599  
Query Match 92.28; Score 142; DB 1; Length 585;  
Best Local Similarity 95.08; Pred. No. 3,27e-16;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 146 NMEADQPONLEETLHCOT 165  
|||||  
QY 1 NMEADQPONLEETLHCOT 20  
RESULT 5  
ENTRY 159173 #type complete  
TITLE glutamate decarboxylase - rat  
ALTERNATE\_NAMES #formal\_name Rattus norvegicus #common\_name Norway rat  
ORGANISM 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change  
DATE 22-Jun-1999  
ACCESSIONS 159173  
REFERENCE 159173  
#authors Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775  
#title Developmentally regulated expression of an exon containing a  
stop codon in the gene for glutamic acid decarboxylase.  
#cross-references MIMD:91062362  
#accession I59173  
##status preliminary; translated from GB/EMBL/DBJ  
##molecule\_type mRNA  
##residues 1-223 #label RES  
##cross-references GB:M8350; NID:g204231; PIDN:AAA41185.1; PID:g204232  
CLASSIFICATION #superfamily human glutamate decarboxylase  
SUMMARY #length 223 #molecular-weight 25069 #checksum 1388  
Query Match 55.88; Score 86; DB 2; Length 223;  
Best Local Similarity 52.98; Pred. No. 4.02e-04;  
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
Db 156 ELSDPESLEQILVDCR 172  
|||  
QY 3 ELADQPONLEETLHCQ 19  
RESULT 6  
ENTRY S61534 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 62K isoform - mouse  
ALTERNATE\_NAMES glutamic acid decarboxylase  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change  
22-Jun-1999  
ACCESSIONS S61534; S61533  
REFERENCE S61534  
#authors Katarova, Z.; Szabo, G.; Mugnai, E.; Greenspan, R.J.  
#journal Eur. J. Neurosci. (1990) 2:190-202  
#title Molecular identification of the 62 kd form of glutamic acid  
decarboxylase from the mouse.  
#accession S61534  
##molecule\_type mRNA  
##residues 1-585 #label KAT  
##cross-references EMBL:249976  
#experimental\_source brain  
REFERENCE S61533  
#authors Szabo, G.  
#submission submitted to the EMBL Data Library, June 1995  
#accession S61533

##molecule\_type mRNA  
##residues 1-534, 'YQPGDXKANFRWYISNPASQSDIDLETETIERLGDL' #label  
SZA  
##cross-references EMBL:249976; NID:9886686; PIDN:CAA90277.1;  
PID:9886687  
#experimental\_source brain  
#note the differences at the carboxyl end are due to a  
frameshift error  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 585 #molecular-weight 65381 #checksum 5716  
Query Match 55.88; Score 86; DB 2; Length 585;  
Best Local Similarity 52.98; Pred. No. 4.02e-04;  
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
Db 156 ELSDPESLEQILVDCR 172  
|||  
QY 3 ELADQPONLEETLHCQ 19  
RESULT 7  
ENTRY A41367 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - rat  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 12-Jun-1992 #sequence\_revision 23-Mar-1995 #text\_change  
18-Jun-1999  
ACCESSIONS A41367; A43756; JH0195  
REFERENCE A41367  
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;  
Dyrberg, T.; Madsen, O.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
#title Cloning, characterization, and autoimmune recognition of rat  
islet glutamic acid decarboxylase in insulin-dependent  
diabetes mellitus.  
#cross-references MIMD:92020930  
#accession A41367  
##status preliminary  
##molecule\_type mRNA  
##residues 1-593 #label MIC  
##cross-references GB:M76177; NID:g204227; PIDN:AAA41184.1; PID:g204228  
REFERENCE A43756  
#authors Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.  
#journal Brain Res. Mol. Brain Res. (1990) 8:193-198  
#title Characterization of a cDNA coding for rat glutamic acid  
decarboxylase  
#cross-references MIMD:91014554  
#accession A43756  
##status preliminary  
##molecule\_type mRNA  
##residues 1-593 #label WYB  
##cross-references GB:X57573; NID:g56183; PIDN:CAA0801.1; PID:g56184  
#note the authors translated the codon TGT for residue 412 as  
Ser and TCT for residue 413 as Cys  
REFERENCE JH0195  
#authors Julien, J.F.; Samama, P.; Mallet, J.  
#journal J. Neurochem. (1990) 54:703-705  
#title Rat brain glutamic acid decarboxylase sequence deduced from a  
cloned cDNA.  
#cross-references MIMD:90132703  
#accession JH0195  
##molecule\_type mRNA  
##residues 1-102, 'V', 104-283, 'S', 285-286, 'AD', 289-343, 'EA', 346, 'I',  
348-351, 'LE', 354-379, 'R', 381-593 #label UTL  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal  
phosphate  
FEATURE

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404                                #binding_site pyridoxal phosphate (Lys) (covalent)
SUMMARY                            #status predicted
                                   #length 593 #molecular_weight 66640 #checksum 3971

Query Match                        55.8%; Score 86; DB 1; Length 593;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 156 ELSDPHESLEQILVDCR 172
|||||::|||::|:|
OY 3 ELADQPQLIEIIMHCQ 19

RESULT 8
ENTRY S48135 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change
07-May-1999

ACCESSIONS
REFERENCE S48135
AUTHORS Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.;
#journal Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.
#title Ann. Hum. Genet. (1992) 56:255-265
Nucleotide sequence and chromosomal assignment of a cDNA
encoding the large isoform of human glutamate
decarboxylase.
#cros-references MUID:93080286
#accession S48135
##residues_type mRNA
##residues 1-593 ##label REL
##cros-references EMBL:Z22750
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 593 #molecular_weight 66952 #checksum 4836

Query Match                        55.8%; Score 86; DB 2; Length 593;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 156 ELSDPHESLEQILVDCR 172
|||||::|||::|:|
OY 3 ELADQPQLIEIIMHCQ 19

RESULT 9
ENTRY S51776 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
16-Feb-1997

ACCESSIONS
REFERENCE S51776
AUTHORS Johnstone, A.
#submission submitted to the EMBL Data Library, May 1993
#accession S51776
##status preliminary
##molecule_type mRNA
##residues 1-593 ##label JOH
##cros-references EMBL:Z22750
#note this is an unpublished revision to the sequence from
reference S48135
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 593 #molecular_weight 66946 #checksum 4842

Query Match                        55.8%; Score 86; DB 2; Length 593;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 156 ELSDPHESLEQILVDCR 172
|||||::|||::|:|
OY 3 ELADQPQLIEIIMHCQ 19
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RESULT	10
ENTRY	B41935
TITLE	glutamate decarboxylase (EC 4.1.1.15) 1 - human
ALTERNATE_NAMES	glutamate decarboxylase GAD67; L-glutamate 1-carboxylase
ORGANISM	[[format_name Homo sapiens]] #common_name man
DATE	31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999
ACCESSIONS	B41935; JH0805; JH0806; A61406; PQ0157; PQ0158; B41367; A36463; A54778
REFERENCE	A41935
#authors	Bu, D.F.; Eriander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.; Kautman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Todin, A.J.
#journal	Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
#title	Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.
#cross-references	MIMD:92196068
#accession	B41935
#molecule_type	mRNA
#residues	1-594 #label BUI
#cross-references	GB:M81883; NID:g182935; PIDN:AAA62368.1; PID:g182936
#experimental_source	pancreatic islet
#note	sequence extracted from NCBI backbone (NCBI:88006)
REFERENCE	JH0805
#authors	Kawasuti, E.; Morichi, R.; Watanabe, M.; Saich, K.; Charle Brunicardi, F.; Watt, P.C.; Yanaguchi, T.; Mullen, Y.; Azawa, S.; Miyamoto, T.; Nagataki, S.
#journal	Biochem. Biophys. Res. Commun. (1993) 192:1353-1359
#title	Cloning and expression of large isoform of glutamic acid decarboxylase from human pancreas and islets.
#cross-references	MIMD:93282845
#accession	JH0805
#molecule_type	mRNA
#residues	1-17,'N',19-30,'N',32-67,'K',69-115,'L',117-154,'T',156-301,'C',303-476,'G',478-491,'G',493-594 #label KAW
#cross-references	GB:S61899; NID:g385310; PIDN:AAB26538.1; PID:g385311
#experimental_source	pancreatic islet
REFERENCE	JH0806
#authors	Yamashta, K.; Cram, D.S.; Harrison, L.C.
#journal	Biochem. Biophys. Res. Commun. (1993) 192:1347-1352
#title	Molecular cloning of full-length glutamic acid decarboxylase 67 from human pancreas and islets.
#cross-references	MIMD:93282844
#accession	JH0806
#molecule_type	mRNA
#residues	1-67,'K',69-435,'L',437-511,'S',513-594 #label YAM
#cross-references	GB:S61897; NID:g385450; PIDN:AAB26937.1; PID:g385451
#experimental_source	pancreatic islet
REFERENCE	A61406
#authors	Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.
#journal	Lancet (1991) 338:1468-1469
#title	Cloning of large isoform of human brain glutamic acid decarboxylase.
#cross-references	MIMD:9205769
#accession	A61406
#molecule_type	mRNA
#residues	62-67,'K',69-205,'N',207-564,'L',566-594 #label KEL
#experimental_source	brain
REFERENCE	PQ0157
#authors	Cram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C.
#journal	Biochem. Biophys. Res. Commun. (1991) 176:1239-1244
#title	Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets.
#cross-references	MIMD:91248209
#accession	PQ0157
#molecule_type	mRNA
#residues	218-463 #label CK1
#cross-references	GB:M70434
#experimental_source	brain
#accession	PQ0158

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#molecule_type mRNA
##residues      218-234,'K','236-240','N','242-288','H','290-323','L','325-329','D','331-338','L','340-390','S','392-397' ##label CR2
#cross-references GB:M0435; NID:g182941; PIDN:AAA52513.1; PID:g182942
#experimental_source pancreatic islet
REFERENCE
#authors      Mjchelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;
#journal      Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
#title        Cloning, characterization, and autoimmune recognition of rat
               diabetis glutamic acid decarboxylase in insulin-dependent
               diabetes mellitus.
#cross-references MIM:D:92029030
#accession    B41367
##molecule_type mRNA
##residues      317-482,'R','484-594' ##label MITC
REFERENCE
#authors      Persson, H.; Peltto-Huikko, M.; Metsis, M.; Soeder, O.; Brene, S.; Skog, S.; Hoefelt, T.; Ritzén, E.M.
#journal      Mol. Cell. Biol. (1990) 10:4701-4711
#title        Expression of the neurotansmitter-synthesizing enzyme
               glutamic acid decarboxylase in male germ cells.
#cross-references MIM:D:90355986
#accession    A36463
##molecule_type mRNA
##residues      527-594' ##label PER
#cross-references GB:M5574; NID:g182929; PIDN:AAA72938.1; PID:g182930
REFERENCE
#authors      Bu, D.F.; Tobin, A.J.
#journal      Genomics (1994) 21:222-228
#title        The exon-intron organization of the genes (GAD1 and GAD2)
               encoding two human glutamate decarboxylases (GAD-67 and
               GAD-65) suggests that they derive from a common ancestral
               GAD.
#cross-references MIM:D:94375018
#contents     annotation: intron-exon organization
COMMENT       This enzyme (GAD) catalyzes the formation of an inhibitory
               neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
               it has several isoforms, each encoded by a separate gene. GAD has
               also been implicated as an autoantigen in autoimmune disease
               stiff-man syndrome and insulin-dependent diabetes mellitus.
GENETICS
#gene         GDB:GAD1; GAD
##cross-references GDB:119244; OMIM:266100
CLASSIFICATION #map_position 2q31-2q31
                #superfamily human glutamate decarboxylase
KEYWORDS       alternative splicing; carbon-carbon lyase; carboxy-lyase;
                phosphoprotein; pyridoxal phosphate
FEATURE
405            #binding-site pyridoxal phosphate (lys) (covalent)
SUMMARY        #status predicted
                #length 594 #molecular-weight 66924 #checksum 6189
Query Match          55.8%; Score 86; DB 1; Length 594;
Best Local Similarity 52.9%; Pfam No..4.02e-04;
Matches              9; Conservative              7; Indels 0; Gaps 0;
Db                  157 ELSDPESLEQLIVDCR 173
OY                 3 ELADQPONLEITLMHCQ 19
RESULT           11
ENTRY TITLE      JC4065 #type complete
ORGANISM          gluamate decarboxylase (EC 4.1.1.15) 67k chain - pig
DATE              30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
                22-Jun-1999
ACCESSIONS        JC4065
REFERENCE         JC4064
#authors          Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
#journal          Gene (1995) 152:257-260
#title            Sequences of two porcine glutamic acid decarboxylases (65-and
```

```

67-kDa GAD)).
#cross-references MIMD:95137399
#accession JC4065
##molecule_type mRNA
##residues 1-594 ##label SUZ
##cross-references DBJ:D31849; NID:g790966; PIDN:BAA06636.1;
PID:d1007208; PID:g790967
#experimental_source brain
COMMENT This enzyme catalyzes the conversion of glutamic acid into
gamma-amino butyric acid.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
FEATURE
402-405 #domain DOPA decarboxylase binding #status predicted
#label BIN
SUMMARY #length 594 #molecular-weight 66894 #checksum 5491
Query Match 55.8% Score 86; DB 2; Length 594;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Db 157 ELSDPESLEQILVDCR 173
|||:||:||:||:|
OY 3 ELADQPQLVEILLHQC 19
RESULT 12
ENTRY #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
22-Jun-1999
ACCESSIONS S51775
REFERENCE S51775
#authors Johnstone, A.
#submission submitted to the EMBL Data Library, May 1993
#accession S51775
##status preliminary
##molecule_type mRNA
##residues 1-594 ##label JOH
#cross-references EMBL:222750; NID:g298098; PIDN:CAA80435.1;
PID:g298099
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 594 #molecular-weight 66973 #checksum 6437
Query Match 55.8% Score 86; DB 2; Length 594;
Best Local Similarity 52.9%; Pred. NO. 4.02e-04;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Db 157 ELSDPESLEQILVDCR 173
|||:||:||:||:|
OY 3 ELADQPQLVEILLHQC 19
RESULT 13
ENTRY #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - cat
ALTERNATE_NAMES glutamate decarboxylase Cmdb7; L-glutamate 1-carboxy-lyase
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
ACCESSIONS A46758
REFERENCE A46758
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#submission Submitted to Genbank, September 1989
#accession A46758
#molecule_type mRNA
##residues 1-594 ##label KOB
#cross-references GB:M8629; NID:g163858; PIDN:AAA51430.1; PID:g163859
A46771
Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
J. Neurosci. (1987) 7:2766-2772
#journal

```

#title	Glutamic acid decarboxylase CDGN: nucleotide sequence encoding an enzymatically active fusion protein.
#cross-references MIMD:87310623	
#accession A43671	
#molecule_type MENA	
#residues 1-558,'RGTRPFGSGSSRPQLSHPLTSSSR','#label KO2	this sequence has been revised in reference A46758
#note This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.	
GENETICS GADI	
#gene #superfamily human glutamate decarboxylase	
CLASSIFICATION carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal	
KEYWORDS phosphate	
FEATURE #binding-site pyridoxal phosphate (lys) (covalent)	
405 #status predicted	
SUMMARY #length 594 #molecular-weight 66824 #checksum 5630	
Query Match 55.8%; Score 86; DB 1; Length 594;	
Best Local Similarity 52.9%; Pred. No. 4.02e-04;	
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;	
DB 157 ELSDPESLEILVDCR 173   :  :: :: :: :	
GK ELADQPNLLETLMHCQ 19	

RESULT	14	S68434	#type complete
ENTRY		FMRamide-activated sodium channel protein,	
TITLE		amloride-sensitive - brown garden snail	
ORGANISM		#formal_name Helix aspersa #common_name brown garden snail	
DATE		17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 24-Sep-1998	
ACCESSIONS		S68434	
REFERENCE		S68434	
#authors		Linsneglia, E.; Champigny, G.; Lazdunski, M.; Barbry, P.	
#journal		Nature (1995) 378:770-773	
#title		Cloning of the amloride-sensitive FMRamide peptide-gated sodium channel.	
#cross-references		MUID:96107314	
#accession		S68434	
##molecule_type	mRNA		
##residues	1-625	#label LIN	
##cross-references	EMBL:X92113; NID:g1149510; PID:e205469; PID:g1149511		
KEYWORDS		glycoprotein; sodium channel; transmembrane protein	
FEATURE			
71-88		#domain transmembrane #status predicted #label TM1\	
537-557		#domain transmembrane #status predicted #label TM2\	
134,196,303,349,			
365,372,473		#binding_site carbohydrate (Asn) (covalent) #status predicted	
SUMMARY		#length 625 #molecular_weight 71350 #checksum 8162	
Query Match		47.4%; Score 73; DB: 2; Length 625;	
Best Local Similarity		58.3%; Pred. No. 1.13e-01;	
Matches	7; Conservative	5; Mismatches 0; Indels 0; Caps 0;	
Db	175 SHNEDMLHCR	186	
Oy	8 PONLEFIMRCO	19	
RESULT	15	T11459	#type complete
ENTRY		Protein P140 - mouse	
TITLE		#formal_name Mus musculus #common_name house mouse	
ORGANISM		20-Sep-1989 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999	
DATE			
ACCESSIONS		T11459	
REFERENCE		Z17896	

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#authors      Croci, L.; Bossolasco, M.; Consalez, G.G.
#submitted    Submitted to the EMBL Data Library, December 1997
#accession    T14159
#status       Preliminary; translated from GB/EMBL/DDBU
##molecule_type mRNA
##residues    1-1216 ##label CRO
#cross-references EMBL:AF040944; NID:g3098417; PID:g3098418;
                  PIDs:NAC15635.1

GENERIC
#note         PI40
SUMMARY       #length 1216 #molecular-weight 130768 #checksum 9650

Query Match          42.9%   Score 66; DB 2; Length 1216;
Best Local Similarity 37.5%; Pred. NO. 1.91e+00;
Matches 6; Conservative 7; Mismatches 3; Indels 0; Caps 0;
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Search completed: Tue Mar 7 21:26:06 2000  
Job time : 8 secs.

\*\*\*\*\*  
 W O R L D  
 (TM)  
 \*\*\*\*\*

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Mparch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Mar 7 21:23:40 2000; Maspar time 3.50 Seconds  
 170.742 Million cell updates/sec  
 Tabular output not generated.

Title: >US-08-981-824-3  
 Description: (1-20) from US08981824.pep  
 Perfect Score: 154  
 Sequence: 1 NMEIADQPQNLEETLMHCQT 20

Scoring table:  
 PAM 150  
 Gap 15

Searched: 82229 segs, 29864866 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database:  
 swiss-prot38  
 1:swissprot

Statistics  
 Mean -29.965; Variance 40.389; scale 0.742

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	154	100.0	585	1	DCE2_PIG	1.14e-21
2	154	100.0	585	1	DCE2_HUMAN	1.14e-21
3	142	92.2	585	1	DCE2_MOUSE	1.53e-18
4	142	92.2	585	1	DCE2_RAT	1.53e-18
5	86	55.8	593	1	DCE1_MOUSE	4.77e-05
6	86	55.8	593	1	DCE1_RAT	4.77e-05
7	86	55.8	594	1	DCE1_PIG	4.77e-05
8	86	55.8	594	1	DCE1_HUMAN	4.77e-05
9	86	55.8	594	1	DCE1_HUMAN	4.77e-05
10	82	53.2	368	1	OXDA_PHOTO	3.45e-04
11	73	47.4	625	1	PANR_HELAS	2.47e-02
12	65	42.2	341	1	OXDD_HUMAN	8.57e-01
13	65	42.2	1356	1	HEP1_PODAN	1.31e+00
14	64	41.6	183	1	60S_RIBOSOMAL_PROTEIN	1.31e+00
15	64	41.6	503	1	VS16_TRYBB	1.31e+00
16	64	41.6	664	1	VP2_BPPH6	1.31e+00
17	63	40.9	183	1	R172_YEAST	1.99e+00
18	63	40.9	332	1	RADA_METJA	1.99e+00
19	63	40.9	468	1	YG4K_YEAST	1.99e+00
20	63	40.9	510	1	SYK_SYNJ3	1.99e+00
21	63	40.9	560	1	PHAC_PSEOL	1.99e+00
22	62	40.3	547	1	YHBX_ECOLI	3.01e+00
23	62	40.3	2515	1	TUD_DROME	3.01e+00

ID	RESULT	1	STANDARD	PRT	585 AA.
24	DCE2_PIG	39.6	209	1	MGMT_CRIGR
25	P48321	39.6	431	1	HYTH_YEAST
26	01-FEB-1996 (Rel. 33, Last sequence update)	39.6	589	1	ARSE_HUMAN
27	01-FEB-1996 (Rel. 33, Last annotation update)	39.6	669	1	ZEAXANTHIN_EPOXIDASE_P
28	GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)	39.0	184	1	YEAD_HAEIN
29	GAD2 OR GAD65.	39.0	228	1	LCK_AEDAE
30	Sus scrofa (Pig).	39.0	484	1	UL32_HSV6U
31	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	39.0	494	1	RNHL_CRIFA
32	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	39.0	627	1	FLGK_BORBU
33	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	39.0	660	1	ZEAXANTHIN_EPOXIDASE_P
34	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	39.0	663	1	ABAZ_NICPL
35	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	39.0	1048	1	NMD5_YEAST
36	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	38.3	1329	1	HOLB_BACSU
37	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	38.3	331	1	CG12_HUMAN
38	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	38.3	341	1	OXDD_BOVIN
39	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	38.3	2044	1	CCAH_HUMAN
40	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	37.7	370	1	POTF_ECOLI
41	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	37.7	507	1	LCK_CHICK
42	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	37.7	749	1	STA_MOUSE
43	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	37.7	1025	1	ITAB_HUMAN
44	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	37.7	1035	1	MT10_YEAST
45	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	37.7	3587	1	SRF1_BACSU

## ALIGNMENTS

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.14e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 CC EMBL: D11848; BAA06635.1; -  
 CC PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 CC PFAM: PF00282; pyridoxal\_dec; 1.  
 CC Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 CC Pyridoxal phosphate; Multigene family;  
 CC FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 CC SEQ SEQUENCE 585 AA; 6538 MW; F3E9BD88 CRC32;

DB 146 NMELADQPONLEILMHCQT 165  
 OY 1 NMELADQPONLEILMHCQT 20

RESULT 2  
 ID DCE2\_HUMAN STANDARD: PRT: 585 AA.  
 AC 005329:  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 DE (65 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD2 OR GAD65.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92196068.  
 RA BU D.-F., ERLANDER M.G., HITZ B.C., TILAKARATNE N.J., KAUFMAN D.L.,  
 RA WAGNER-MCHERSON C.B., EVANS G.A., TOBIN A.J.;  
 RT "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are  
 RT each encoded by a single gene."  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 94375018.  
 RA BU D.-F., TOBIN A.J.;  
 RT "The exon-intron organization of the genes (GAD1 and GAD2) encoding  
 RT two human glutamate decarboxylases (GAD67 and GAD65) suggests that  
 RT they derive from a common ancestral GAD."  
 RL Genomics 21:222-228(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE-PANCREATIC ISLETS;  
 RX MEDLINE: 92020848.  
 RA KALISN A.E., MAGOPAN W.A., GRUBIN C.E., DUBE S., DISTECHE C.M.,  
 RA ADLER D.A., BARREITER H., MATHEWS S., GRANT F.J., FOSTER D.,  
 RA LERNMARK A.;  
 RT "Cloning and primary structure of a human islet isoform of glutamic  
 RT acid decarboxylase from chromosome 10."  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).  
 RL [4]  
 RN SEQUENCE OF 6-585 FROM N.A.  
 RX TISSUE-PANCREAS;  
 RX MEDLINE: 93185681.  
 RA MARCHEL L., ABNEY C.C., BERG H., SCHERBAUM W.A., LIEVOGEL B.,  
 RA NORTHEMAN W.;  
 RT "Characterization of a linear epitope within the human pancreatic  
 RT 64-kDa glutamic acid decarboxylase and its autoimmune recognition by  
 RT sera from insulin-dependent diabetes mellitus patients."  
 RL Eur. J. Biochem. 212:597-603(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 CC DECARBOXYLASE.  
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 CC -----  
 CC EMBL: M81882; AAA62367.1; -  
 CC DR EMBL: M74826; AAA58491.1; -  
 CC DR EMBL: X69936; CAA49554.1; ALT\_INIT.  
 CC DR EMBL: M70435; AAA52513.1; -  
 CC PIR: A41292; A41292.

DR PIR: P00158; P00158.  
 DR MIR: 138275; -  
 DR PROSITE; PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM; PF00282; pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 396 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 585 AA; 65411 MW; 8AD62B62 CRC32.

Query Match 100.0%; Score 154; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1,14e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 146 NMELADQPONLEILMHCQT 165  
 OY 1 NMELADQPONLEILMHCQT 20

RESULT 3  
 ID DCE2\_MOUSE STANDARD: PRT: 585 AA.  
 AC P48320; 035519;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUN-1998 (Rel. 36, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 DE (65 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD2 OR GAD65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE: 94032481.  
 RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;  
 RT "Cloning and sequence analysis of a murine cDNA encoding glutamate  
 RT decarboxylase (GAD65)."  
 RL Biochim. Biophys. Acta 1216:157-160(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE: 97115675.  
 RA ASADA H., KAWAMURA Y., MARYAMA K., KUME H., DING R.G., JI F.Y.,  
 RA KANBARA N., KUZUME H., SANBO M., YAGI T., OBATA K.;  
 RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase  
 RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but  
 RT are susceptible to seizures."  
 RL Biochem. Biophys. Res. Commun. 229:891-895(1996).  
 RN [3]  
 RP SEQUENCE OF 175-379 FROM N.A.  
 RX TISSUE-BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localization and quantitation of expression of two glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat."  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 CC DECARBOXYLASE.  
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 CC -----  
 CC EMBL: L16980; AAA93049.1; -



DR EMBL: D42051: BAA22893.1: -  
DR EMBL: S67454: CAB32806.1: -  
DR MGD: MGI:95634: GAD2.  
DR PROSITE: PS00392: DDC\_GAD\_HDC\_YDC: 1.  
DR PFM: PF00282: Pyridoxal\_dec: 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family;  
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).  
FT CONFLICT 259 259 F -> S (IN REF. 2).  
FT CONFLICT 319 319 I -> S (IN REF. 3).  
FT CONFLICT 325 325 K -> E (IN REF. 2).  
FT CONFLICT 499 499 P -> S (IN REF. 2).  
SQ SEQUENCE 585 AA: 65224 MW: 9855088 CRC32:  
Query Match 92.2%; Score 142; DB 1; Length 585;  
Best Local Similarity 95.0%; Pred. No. 1.53e-18;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Db 146 NWEIADOPONLEILTHCOT 165  
OY 1 NWEIADOPONLEILTHCOT 20  
RESULT 4  
ID DCE2 RAT STANDARD: PRT: 585 AA.  
AC O05683:  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).  
OS GAD2 OR GAD65.  
NS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-HIPPOCAMPUS;  
RA MEDLINE: 91299343.  
RA ERLANDER M.G., TILAKARATNE N.J., FELDBLUM S., PATEL N.,  
RA TOBIN A.J.:  
RT "Two genes encode distinct glutamate decarboxylases."  
RL Neuron 7:91-100(1991).  
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE -> 4-AMINOBUTANOATE + CO(2).  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
DECARBOXYLASE.  
CC -----  
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CC -----  
DR EMBL: M72422: AAA63488.1: -  
DR PROSITE: PS00392: DDC\_GAD\_HDC\_YDC: 1.  
DR PFM: PF00282: Pyridoxal\_dec: 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family.  
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).  
SQ SEQUENCE 585 AA: 65402 MW: E35D601A CRC32:

RESULT 5  
ID DCE1 MOUSE STANDARD: PRT: 593 AA.  
AC P48318:  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
GN GAD1 OR GAD67.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA KATAROVA Z., SZABO G., MUGNAINI E., GREENSPAN R.;  
RT "Molecular identification of the 62 kd form of glutamic acid  
RT decarboxylase from the mouse."  
RL Eur. J. Neurosci. 2:190-202(1990).  
RN [2]  
RP SEQUENCE OF 198-403 FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE: 94062679.  
RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.:  
RT "Localization and quantitation of expression of two glutamate  
RT decarboxylase genes in pancreatic beta-cells and other peripheral  
RT tissues of mouse and rat."  
RL Endocrinology 133:2962-2972(1993).  
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE -> 4-AMINOBUTANOATE + CO(2).  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
CC TYRDC).  
CC -----  
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CC -----  
DR EMBL: 249976: CA90277.1: -  
DR EMBL: S67453: CAB32805.1: -  
DR MGD: MGI:95632: GAD1.  
DR PROSITE: PS00392: DDC\_GAD\_HDC\_YDC: 1.  
DR PFM: PF00282: Pyridoxal\_dec: 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family.  
FT BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).  
FT CONFLICT 234 234 E -> K (IN REF. 2).  
FT CONFLICT 258 258 S -> T (IN REF. 1).  
FT CONFLICT 360 360 D -> S (IN REF. 1).  
SQ SEQUENCE 593 AA: 66584 MW: 63BC57AA CRC32:  
Query Match 55.8%; Score 86; DB 1; Length 593;  
Best Local Similarity 52.9%; Pred. No. 4.77e-05;  
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;  
Db 156 ELSDHPSLEQIIVDCR 172  
OY 3 ELADOPONLEILTHCOT 19  
RESULT 6  
ID DCE1 RAT STANDARD: PRT: 593 AA.  
AC P18088:  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)







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FT CARBOHYD 134 134 POTENTIAL.
FT CARBOHYD 196 196 POTENTIAL.
FT CARBOHYD 303 303 POTENTIAL.
FT CARBOHYD 349 349 POTENTIAL.
FT CARBOHYD 365 365 POTENTIAL.
FT CARBOHYD 372 372 POTENTIAL.
FT CARBOHYD 473 473 POTENTIAL.
SQ SEQUENCE 625 AA: 71350 MW: 8D25C3F3 CRC32:

Query Match
Best Local Similarity 58.3%; Score 73; DB 1; Length 625;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 175 SHNEDMLMHC 186
QY 8 PONTLEELMHQC 19

RESULT 12
ID OXDP_HUMAN STANDARD: PRT; 341 AA.
AC 099489;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE D-ASPARTATE OXIDASE (EC 1.4.3.1) (DASOX) (DDO).
GN DDO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 97306065.
RA SETOYAMA C., MURA R.;
RT "Structural and functional characterization of the human brain D-
RT aspartate oxidase."
RL J. Biochem. 121:798-803(1997).
CC -1- FUNCTION: SELECTIVELY CATALYZES THE OXIDATIVE DEMINATION OF D-
CC ASPARTATE AND ITS N-METHYLATED DERIVATIVE, N-METHYL D-ASPARTATE.
CC -1- CATALYTIC ACTIVITY: D-ASPARTATE + H(2)O + O(2) = OXALACETATE +
CC NH(3) + H(2)O(2).
CC -1- COFACTOR: FAD OR 6-HYDROXYFLAVIN ADENINE DINUCLEOTIDE.
CC -1- SUBCELLULAR LOCATION: PEROXISOMAL.
CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS, DDO-1 (SHOWN HERE) AND DDO-2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE DAMOX/DASOX FAMILY.
CC -----
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CC -----
CC EMBL: D89858; BAA14031.1; -
CC HSSP: P00371; IDAO.
CC DR MIM: 124450; -
CC DR PROSITE: PS00677; DAO: 1.
CC DR PFAM: PF01266; DAO: 1.
CC KM OXidoreductase; Flavoprotein; FAD; Peroxisome; Alternative splicing.
FT NP_BIND 6 20 FAD (ADP PART) (POTENTIAL).
FT ACT_SITE 223 223 BY SIMILARITY.
FT ACT_SITE 302 302 BY SIMILARITY.
FT SITE 339 341 MICROBODY TARGETING SIGNAL (POTENTIAL).
FT VARSPLIC 95 153 MISSING (IN ISOFORM DDO-2).
SQ SEQUENCE 341 AA: 37535 MW: 0948D6AB CRC32:

Query Match
Best Local Similarity 42.2%; Score 65; DB 1; Length 341;
Matches 7; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db 241 DMLSPDAENSRILSNC 258
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QY 1 MWELADDPONTLEELMHQC 18

RESULT 13
ID HETL_PODAN STANDARD: PRT; 1356 AA.
AC 000808;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.
GN HET-E1.
OS Podospora anserina.
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
OC Sordariales; Sordariaceae; Podospora.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96009891.
RA SAUPE S., TURCO B., BEGUERET J.;
RT "A gene responsible for vegetative incompatibility in the fungus
RT Podospora anserina encodes a protein with a GTP-binding motif and G
RT beta homologous domain."
RL Gene 162:135-139(1995).
CC -1- FUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH
CC SPECIFIC INTERACTIONS WITH DIFFERENT ALLELES OF THE UNLINKED GENE,
CC HET-C.
CC -1- SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS).
CC -----
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CC -----
CC EMBL: L28125; AAA85775.1; -
CC DR PROSITE: PS00678; WD_REPEATS: 10.
CC DR PFAM: PF00400; WD40; 10.
CC KW GTP-Binding; Repeat; WD repeat.
FT NP_BIND 300 307 GTP (POTENTIAL).
FT REPEAT 839 869 WD1.
FT REPEAT 881 911 WD2.
FT REPEAT 923 953 WD3.
FT REPEAT 965 995 WD4.
FT REPEAT 1007 1037 WD5.
FT REPEAT 1049 1079 WD6.
FT REPEAT 1091 1121 WD7.
FT REPEAT 1133 1163 WD8.
FT REPEAT 1175 1205 WD9.
FT REPEAT 1217 1247 WD10.
SQ SEQUENCE 1356 AA: 149765 MW: 96B8E37B CRC32:

Query Match
Best Local Similarity 42.2%; Score 65; DB 1; Length 1356;
Matches 7; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 585 DVSDDPESEIEYKLC 600
QY 3 ELADDPONTLEELMHQC 18

RESULT 14
ID R171_YEAST STANDARD: PRT; 183 AA.
AC P05740;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 60S RIBOSOMAL PROTEIN L17-A (YL17-A).
GN RPL17A OR RPL17 OR YKL180W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
```

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RN [1]
RP SEQUENCE FROM N.A.
RA WIMMANN S., VOSS H., SCHWAGER C., RUPP T., GROTHUES D., SENSEN C.,
RA STEGEMANN J., ZIMMERMANN J., ERFLE H., HEWITT N., ANSORGE W.;
RL Submitted (MAR-1994) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-113 FROM N.A.
RX MEDLINE: 94205264.
RA WIMMANN S., VOSS H., SCHWAGER C., RUPP T., STEGEMANN J.,
RA ZIMMERMANN J., GROTHUES D., SENSEN C., ERFLE H., HEWITT N.,
RA BARREY A., ANSORGE W.;
RT "Sequencing and analysis of 51.6 kilobases on the left arm of
RT chromosome XI from Saccharomyces cerevisiae reveals 23 open reading
RT frames including the FAS1 gene."
RL Yeast 9:1343-1348(1993).
RN [3]
RP PRELIMINARY SEQUENCE OF 1-40.
RA OTAKA E., HIGO K.-I., ITOH T.;
RT "Yeast ribosomal proteins: VIII. Isolation of two proteins and
RT sequence characterization of twenty-four proteins from cytoplasmic
RT ribosomes."
RL Mol. Gen. Genet. 195:544-546(1984).
CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR L17 IN YEAST.
CC -1- SIMILARITY: BELONGS TO THE L22P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: Z28180; CA82023.1; -
DR EMBL: Z28179; CA82022.1; -
DR EMBL: X74151; CAA52258.1; -
DR PIR: S38012; S38012.
DR HSSP: P48286; 1BXE.
DR SGD: L0001715; RPL17A.
DR PROSITE: PS00464; RIBOSOMAL_L22; 1.
DR PFAM: PF00237; Ribosomal_L22; 1.
KW Ribosomal protein; Multigene family.
FT INIT_MET 0
FT CONFLICT 0
FT SEQUENCE 103 AA; 20418 MW; C00DA5F7 CRC32;
SQ
Query Match 41.6%; Score 64; DB 1; Length 183;
Best Local Similarity 43.8%; Pred. No. 1.31e+00;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Db 38 WELTRAKRYLEQVLGH 53
OY 2 WELADOPQNLIELIMH 17

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RESULT 15
ID VS16_TRYBB STANDARD: PRT: 503 AA.
AC P06014;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE VARIANT SURFACE GLYCOPROTEIN ILTAT 1.3 PRECURSOR (VSG).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE FROM N.A.
RA RICE-FICHT A.C., CHEN K.K., DONELSON J.E.;
RT "Sequence homologies near the C-termini of the variable surface
RT glycoproteins of Trypanosoma brucei."
RL Nature 294:53-57(1981).
CC -1- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE
CC TYRANOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING
CC A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000

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CC VSG GENES.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A
CC PI-PLC.
CC -----
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CC -----
DR EMBL: J01221; AAA30288.1; -
DR PIR: S09640; S09640.
DR PFAM: PF00913; Trypan_glycop. 1.
KW Glycoprotein; Antigen; Trypanosomatids; Signal; GPI-anchor; Membrane.
FT SIGNAL 1 29
FT CHAIN 30 480
FT PROPEP 481 503
FT DISULFID 42 168
FT CARBOHYD 150 206
FT CARBOHYD 419 419
FT CARBOHYD 432 432
FT LIPID 480 480
FT SEQUENCE 503 AA; 54618 MW; 399B4ECE CRC32;
SQ
Query Match 41.6%; Score 64; DB 1; Length 503;
Best Local Similarity 41.2%; Pred. No. 1.31e+00;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
Db 304 NWKPADKPNADYLIKQ 320
OY 1 NWELADOPQNLIELIMH 17

```

Search completed: Tue Mar 7 21:23:47 2000  
Job time : 7 secs.

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**MPsrch\_pp** protein - protein database search, using Smith-Waterman algorithm

```
Run on:      Tue Mar  7 21:24:04 2000;      MasPar time 9.55 Seconds
Tabular output not generated.      145.246 Million cell updates/sec
```

Title:	>US-08-981-824-3
Description:	(1-20) from US08981824.pep
Perfect Score:	154
Sequence:	1 MWELADQPONLLEFIIMHCQT 20

Scoring table: PAM 150  
Gap 15

Searched: ~~225878~~ seqs, 69334122 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle  
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified  
13:sp\_vertebrate 14:sp\_virus

~~Statistics:~~ Mean 28.911; Variance 38.261; scale 0.756

~~Pred. No.~~ is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	86	55.8	223	11	063211	GLUTAMATE DECARBOXYLAS	3.82e-05
2	86	55.8	593	11	008685	67KD GLUTAMIC ACID DEC	3.82e-05
3	82	53.2	590	13	09Y158	GLUTAMATE DECARBOXYLAS	2.97e-04
4	66	42.9	547	2	Q46594	OUTER MEMBRANE ADHEREN	6.46e-01
5	66	42.9	1216	11	070298	P140.	6.46e-01
6	64	41.6	296	5	003356	F35E12.3 PROTEIN.	1.57e+00
7	64	41.6	515	2	053215	TRANSPOSASE.	1.57e+00
8	64	41.6	547	2	P74269	ALPHA-ISOPROPYLMATE	1.57e+00
9	64	41.6	3229	5	Q26912	PROTEIN 1 OF A DISPERS	1.57e+00
10	63	40.9	162	1	Q9ICX4	162AA LONG HYPOTHETICA	2.44e+00
11	63	40.9	533	2	Q9E435	POLY(HYDROXYALKANATE)	2.44e+00
12	63	40.9	652	10	Q9ZT78	HYPOTHETICAL 72.0 KD P	2.44e+00
13	63	40.9	655	1	Q27929	CONSERVED PROTEIN.	2.44e+00
14	63	40.9	1033	5	Q24327	GP160-DTRK PRECURSOR.	2.44e+00
15	62	40.3	221	14	012175	ENVELOPE GLYCOPROTEIN	3.76e+00
16	62	40.3	221	14	013168	ENVELOPE GLYCOPROTEIN	3.76e+00
17	62	40.3	492	10	Q9Z5Y9	HYDROPEROXIDE LIASE.	3.76e+00
18	62	40.3	1665	4	Q94898	KIAA806 PROTEIN.	3.76e+00
19	61	39.6	347	10	082357	PUTATIVE 3-METHYL-2-OX	5.78e+00
20	61	39.6	595	3	Q94419	HYPOTHETICAL 68.1 KD P	5.78e+00

21	6	39.6	792	4	095802	SMAP.	5.78e+00
22	61	39.6	793	11	P70188	KINESIN-ASSOCIATED PRO	5.78e+00
23	61	39.6	1360	13	Q9YGS5	PEG7.	5.78e+00
24	61	39.6	1364	14	Q9YHG6	13S CONDENSIN XCAP-D2	5.78e+00
25	61	39.6	2457	14	Q41965	TEGUMENT PROTEIN.	5.78e+00
26	61	39.6	5327	5	Q76891	EG-49E4.1 PROTEIN.	5.78e+00
27	60	39.0	479	5	Q44505	ROD3.7 PROTEIN.	8.82e+00
28	60	39.0	512	14	Q69059	HERPESVIRUS 6 IMMEDIAT	8.82e+00
29	60	39.0	669	2	Q87518	EXOGENOUS FERRIC SIDER	8.82e+00
30	60	39.0	1751	14	Q87815	PR GAG-PRO-POL.	8.82e+00
31	59	38.3	192	2	P74092	HYPOTHETICAL 19.1 KD P	1.34e+01
32	59	38.3	170	2	Q9XW2	CONSERVED HYPOTHETICAL	1.34e+01
33	59	38.3	320	2	Q07727	PROBABLE AMINO ACID OX	1.34e+01
34	59	38.3	324	5	Q45313	C5AE10.2 PROTEIN.	1.34e+01
35	59	38.3	339	3	Q09387	HYPOTHETICAL 38.0 KD P	1.34e+01
36	59	38.3	339	3	Q14024	HYPOTHETICAL 39.9 KD P	1.34e+01
37	59	38.3	362	10	Q81811	PUTATIVE PHYCOELATIN	1.34e+01
38	59	38.3	388	2	Q52552	3-AMINO-5-HYDROXYBENZ	1.34e+01
39	59	38.3	388	2	Q44095	3-AMINO-5-HYDROXY BENZ	1.34e+01
40	59	38.3	414	2	Q64258	HYPOTHETICAL 45.8 KD P	1.34e+01
41	59	38.3	539	3	Q14000	CHROMOSOME IV READING	1.34e+01
42	59	38.3	885	3	Q07533	PURHOSOME IV READING	1.34e+01
43	59	38.3	1214	4	Q9Y4C7	KIAA0690 PROTEIN (FRAG	1.34e+01
44	59	38.3	1430	5	Q2350	KZ783.4 PROTEIN	1.34e+01
45	59	38.3	2353	4	Q95802	LOW-VOLTAGE ACTIVATED	1.34e+01

RESULT	1	ALIGNMENTS
ID	Q63211	PRT: 223 AA.
AC	Q63211	
DT	01-NOV-1996 (TREMblrel. 01, Created)	
DT	01-NOV-1996 (TREMblrel. 01, Last sequence update)	
DT	01-NOV-1998 (TREMblrel. 08, Last annotation update)	
DE	GLUTAMATE DECARBOXYLASE.	
OS	Rattus norvegicus (Rat).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE; 91062362.	
RA	BOND R.W., WYBORSKI R.J., GOTTLIEB D.I.;	
RT	"Developmentally regulated expression of an exon containing a stop	
RT	codon in the gene for glutamate acid decarboxylase."	
RL	Proc. Natl. Acad. Sci U.S.A. 87:8771-8775(1990).	
DR	EMBL; M38350; AAA41183.1; -;	
DR	PFAM; PF00282; pyridoxal_dec; 1.	
DR	SEQUENCE 223 AA; 25069 MW; C7162AC1 CRC32;	

QY	Query Match	55.8%;	Score 86;	DB 11;	Length 223;
DB	Best Local Similarity	52.9%;	Pred. NO. 3.82e-05;		
QY	Matches 9;	Conservative 7;	Mismatches 1;	Indels 0;	Gaps 0
DB	156 ELSDHPESLEILVDCR 172				
QY	: : : : : : : : :				
	3 ELADPQNLLEILMHQC 19				

RESULT	2	PRELIMINARY:	PRT: 593 AA.
ID	Q06885		
AC	Q06885;		
DT	01-JUL-1997 (TREMblrel. 04, Created)		
DT	01-JUL-1997 (TREMblrel. 04, Last sequence update)		
DT	01-NOV-1999 (TREMblrel. 12, Last annotation update)		
DE	67KD GLUTAMIC ACID DECARBOXYLASE.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RP	SEQUENCE FROM N.A.		
RX	STRAIN-BALB/C;		
RA	AUST G., STEINBRENNER H., THAMM B., ROST A.K., SESSLER J.;		

Db 235 RDVIDSNSNLESVLIQC 251



QY 2 WELADOPONLEIIMHC 18

RESULT 7 PRELIMINARY: PRT: 515 AA.

AC 052215;  
DT 01-JUN-1998 (TIREMBLrel. 06, Created)  
DT 01-JUN-1998 (TIREMBLrel. 06, Last sequence update)  
DT 01-AUG-1998 (TIREMBLrel. 07, Last annotation update)  
DE TRANSPORTASE.  
OS Pseudomonas pseudocataligenes.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;  
RN Pseudomonas.  
RP SEQUENCE FROM N.A.  
RC STRAIN-JS45;  
RA DAVIS J.K., SOMERVILLE C.C., SPAIN J.C.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF028594; AAB94124.1;  
SQ SEQUENCE 515 AA; 56566 MW; 1BAE619 CRC32;

Query Match 41.6%; Score 64; DB 2; Length 515;  
Best Local Similarity 38.5%; Pred. No. 1.57e+00;  
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 499 DWDLAOPDEVDO 511  
QY 1 NWEADOPONLEI 13

RESULT 8 PRELIMINARY: PRT: 547 AA.  
AC P74269;  
DT 01-FEB-1997 (TIREMBLrel. 02, Created)  
DT 01-FEB-1997 (TIREMBLrel. 02, Last sequence update)  
DT 01-JAN-1999 (TIREMBLrel. 09, Last annotation update)  
DE ALPHA-ISOPROPYLMALATE SYNTHASE.  
GN LEUA.  
OS Synechocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PCC6803;  
RA TABATA S.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-PCC6803;  
RX MEDLINE; 97061201.  
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,  
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,  
RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARIO K., OKUMURA S.,  
RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M.,  
RA TABATA S.;  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
RT entire genome and assignment of potential protein-coding regions.";  
RL DNA Res. 3:109-136(1996).  
DR EMBL; D90913; BAA18363.1;  
DR PFAM; PF00882; HMG-Like; 1.  
SQ SEQUENCE 547 AA; 59819 MW; 6FDA2E7C CRC32;

Query Match 41.6%; Score 64; DB 2; Length 547;  
Best Local Similarity 36.8%; Pred. No. 1.57e+00;  
Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 62 WOLOEPLEQAEIVACST 80  
QY 2 WELADOPONLEIIMHCOT 20

RESULT 9

ID 026912 PRELIMINARY: PRT: 3229 AA.

AC 026912;  
DT 01-NOV-1996 (TIREMBLrel. 01, Created)  
DT 01-NOV-1996 (TIREMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TIREMBLrel. 08, Last annotation update)  
DE PROTEIN 1 OF A DISPERSED GENE FAMILY (DGF-1).  
GN DGF-1.  
OS Trypanosoma cruzi.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 93063053.  
RA WINCKER P., MURTA-DOVALES A.C., GOLDBERG S.;  
RT "Nucleotide sequence of a representative member of a Trypanosoma cruzi  
RT dispersed gene family.";  
RL Mol. Biochem. Parasitol. 55:217-220(1992).  
DR EMBL; M90534; AAA30182.1;  
SQ SEQUENCE 3229 AA; 334929 MW; F75E94C3 CRC32;

Query Match 41.6%; Score 64; DB 5; Length 3229;  
Best Local Similarity 35.3%; Pred. No. 1.57e+00;  
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 730 WTFNAPQOTNITLHC 746  
QY 2 WELADOPONLEIIMHC 18

RESULT 10 PRELIMINARY: PRT: 162 AA.  
AC 09YCX4;  
DT 01-NOV-1999 (TIREMBLrel. 12, Created)  
DT 01-NOV-1999 (TIREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TIREMBLrel. 12, Last annotation update)  
DE 162AA LONG HYPOTHETICAL PROTEIN.  
GN APEL138.  
OS Aeropyrum pernix.  
OC Archaea; Crenarchaeota; Aeropyrum.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K1;  
RX MEDLINE; 99310339.  
RA KAWARABAYASHI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,  
RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,  
RA HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,  
RA TAKAMURA M., MASUDA S., FUNAHASHI T., TANAKA T., KUOH Y.,  
RA YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,  
RA NOMURA N., SAKO Y., KIRUCHI H.;  
RT "Complete genome sequence of an aerobic hyper-thermophilic  
RT crenarchaeon, Aeropyrum pernix K1.";  
RL DNA Res. 6:83-101(1999).  
DR EMBL; AP000060; BAA80123.1;  
SQ SEQUENCE 162 AA; 17732 MW; 90001DD CRC32;

Query Match 40.9%; Score 63; DB 1; Length 162;  
Best Local Similarity 43.8%; Pred. No. 2.44e+00;  
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 9 WKLEQSESELEIAR 24  
QY 2 WELADOPONLEIIMH 17

RESULT 11 PRELIMINARY: PRT: 533 AA.  
AC 09Z435;  
DT 01-MAY-1999 (TIREMBLrel. 10, Created)  
DT 01-MAY-1999 (TIREMBLrel. 10, Last sequence update)  
DT 01-MAY-1999 (TIREMBLrel. 10, Last annotation update)  
DE POLY(HYDROXYALKANONATE) SYNTHASE (FRAGMENT).  
GN PHAC2.  
OS Pseudomonas putida.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;

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OC Pseudomonas.
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN-BMO1;
RA VALENTIN H.E., STUART E.S., FULLER R.C., LENZ R.W., DENNIS D.;
RT "Investigation of the function of proteins associated to
RT polyhydroxyalkanoate) inclusions in Pseudomonas putida BMO1.";
RL J. Biotechnol. 0:0-0(1998).
DR EMBL: AF042276; AAD02217.1; -.
FT NON_TER
SQ SEQUENCE 533 AA; 59894 MW; E038BD80 CRC32;

Query Match
Best Local Similarity 40.9%; Score 63; DB 2; Length 533;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Db 237 EMBL:AF042276; AAD02217.1; -.
QY 1 NWELADQPONLEILMHCOT 20

RESULT 12
ID 092778 PRELIMINARY; PRT; 652 AA.
AC 092778;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE HYPOTHETICAL 72.0 KD PROTEIN.
GN F9H3.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA.
RA HUANG E.N., PARNELL L.D., DE LA BASTIDE M., SCHUTZ K., HABERMANN K.,
RA DEDHIA N.N., MCCOMBIE W.R.;
RT "Genomic sequence of Arabidopsis thaliana BAC F9H3, chromosome IV,
RT 18.8 cm.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF071527; AAD11592.1; -.
KW Hypothetical protein
SQ SEQUENCE 652 AA; 71969 MW; B5B68A6B CRC32;

Query Match
Best Local Similarity 66.7%; Score 63; DB 10; Length 652;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 326 HVOLEELILMHC 337
QY 7 QPONLEILMHC 18

RESULT 13
ID 027929 PRELIMINARY; PRT; 655 AA.
AC 027929;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE CONSERVED PROTEIN.
GN MTH1907.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RA MEDLINE: 98037514.
RA SMITH D.R., DOUGHERTY-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
RA ALDRIDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTIER B., QIU D.,

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RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA JIRANI N., CARUSO A., BUSH D., SAFER H., PATMELL D., PRAHAAR S.,
RA MCDUGALL S., SHMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL: AE000942; AAB6367.1; -.
SQ SEQUENCE 655 AA; 75562 MW; 05CC7FD2 CRC32;

Query Match
Best Local Similarity 50.0%; Score 63; DB 1; Length 655;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 164 LDRHSELEILM 177
QY 4 LADQPONLEILM 17

RESULT 14
ID 024327 PRELIMINARY; PRT; 1033 AA.
AC 024327;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GP160-DTRK PRECURSOR.
GN DTRK.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN-CANTON S;
RX MEDLINE: 92164624.
RA PULIDO D., CAMPUZANO S., KODA T., MODOLELL J., BARBACID M.;
RT "Dtrk, a Drosophila gene related to the trk family of neurotrophin
RT receptors, encodes a novel class of neural cell adhesion molecule.";
RL EMBL: X63453; CAA45053.1; -.
DR HSSP: P06213; IIRK.
DR FLYBASE: FBgn004839; TK48D.
DR PFAM: PF00047; igf_5.
DR PFAM: PF00069; pkinase; 1.
KW Signal; Cell adhesion.
FT SIGNAL
FT CHAIN 1
SQ SEQUENCE 1033 AA; 114367 MW; 1F8EB944 CRC32;

Query Match
Best Local Similarity 42.1%; Score 63; DB 5; Length 1033;
Matches 8; Conservative 6; Mismatches 4; Indels 1; Gaps 1;

Db 988 EMSVAETPDSLEILSC 1006
QY 1 NWELADQ-PONLEILMHC 18

RESULT 15
ID 012175 PRELIMINARY; PRT; 221 AA.
AC 012175;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
RN [1]
RA SEQUENCE FROM N.A.
RX MEDLINE: 98080455.
RA DEWART E.L., MULLINS J.I., GUPTA P., LEARN G.H. JR., HOLODNIT M.,
RA KATZENSTEIN D., WALKER B.D., SINGH M.K.;

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RT "Human immunodeficiency virus type 1 populations in blood and semen."  
RL J.VIROL.72:617-623(1998).  
DR EMBL: U96510; AAC40359.1; -.  
DR PFWA: PF00516; GP120; 1.  
KW Envelope protein.  
FT NON\_TER 1 1  
FT NON\_TER 221 221  
SQ SEQUENCE 221 AA: 24697 MW: FDB68EB3 CRC32:  
  
Query Match 40.3%; Score 62; DB 14; Length 221;  
Best Local Similarity 27.8%; Pred. No. 3.76e+00;  
Matches 5; Conservative 9; Mismatches 4; Indels 0; Gaps 0;  
  
Db 141 WNTESNNTITLPCR 158  
QY 2 WELADQPONLEILMHCQ 19

Search completed: Tue Mar 7 21:24:16 2000  
Job time : 12 secs.

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 W01796  
 (TM)  
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MPSrch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Mar 7 21:35:51 2000; MasPar time 3.16 Seconds  
 Tabular output not generated. 150.130 Million cell updates/sec

Title: >US-08-981-824-4  
 Description: (1-20) from US08981824.pep  
 Perfect Score: 147  
 Sequence: 1 TLKYAIKTHPRYFNQLSG 20

Scoring table: PAM 150  
 Gap 18

Searched: 188963 segs, 23686106 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: a-geneseq35  
 1:geneseqp

Statistics: Mean 20.522; Variance 63.466; scale 0.323

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	147	100.0	20	1 W01796	Human 65 kD glutamine	3.73e-09
2	147	100.0	20	1 W18845	65 kD glutamic acid de	3.73e-09
3	147	100.0	503	1 R23645	Human GAD65 gene produ	3.73e-09
4	147	100.0	540	1 R59520	GAD65 1-45 N-terminal-	3.73e-09
5	147	100.0	540	1 R59521	GAD65 1-45 N-terminal-	3.73e-09
6	147	100.0	544	1 R59525	GAD65 545-585 C-termi	3.73e-09
7	147	100.0	544	1 R59524	GAD65 545-585 C-termi	3.73e-09
8	147	100.0	554	1 R59518	GAD65 1-31 deleted, C4	3.73e-09
9	147	100.0	554	1 R59519	GAD65 1-31 deleted, C4	3.73e-09
10	147	100.0	584	1 W34520	Rat GAD65 protein.	3.73e-09
11	147	100.0	584	1 W86018	Rat GAD65 protein, sequ	3.73e-09
12	147	100.0	584	1 W86017	Human GAD65 protein se	3.73e-09
13	147	100.0	584	1 W34519	Human GAD65 protein se	3.73e-09
14	147	100.0	585	1 R79105	Human glutamic acid de	3.73e-09
15	147	100.0	585	1 W14915	Modified glutamic acid	3.73e-09
16	147	100.0	585	1 R71641	Human GAD. 65.	3.73e-09
17	147	100.0	585	1 R29629	Human GAD. 65.	3.73e-09
18	147	100.0	585	1 W12402	65 kD human glutamic a	3.73e-09
19	147	100.0	585	1 W14916	Modified glutamic acid	3.73e-09
20	147	100.0	585	1 R23644	Rat GAD65 gene product	3.73e-09
21	147	100.0	585	1 R28756	Human pancreatic islet	3.73e-09
22	147	100.0	585	1 R59517	Rat GAD65.	3.73e-09
23	147	100.0	585	1 W35361	Human 65K-glutamic aci	3.73e-09

24	147	100.0	585	1 R29628	Rat GAD 65.	3.73e-09
25	147	100.0	585	1 R59516	Human GAD65.	3.73e-09
26	147	100.0	593	1 R71733	Rat glutamic acid deca	3.73e-09
27	134	91.2	593	1 R27220	Brain GAD #2.	1.50e-07
28	134	91.2	594	1 R27222	Full length islet GAD.	1.50e-07
29	134	91.2	594	1 R27221	Full length brain GAD.	1.50e-07
30	134	91.2	594	1 W74716	Amino acid sequence of	1.50e-07
31	134	91.2	594	1 W74717	Amino acid sequence of	1.50e-07
32	113	76.9	493	1 W20065	Human GADII protein.	5.24e-05
33	113	76.9	493	1 W22306	Human GADII.	5.24e-05
34	108	73.5	506	1 W20064	Rat GADII protein.	2.06e-04
35	108	73.5	506	1 W22305	Rat GADII.	2.06e-04
36	97	66.0	15	1 W12404	GAD65 residues 173-187	4.03e-03
37	95	64.6	20	1 R72272	Glutamic acid decarbox	6.87e-03
38	79	53.7	20	1 R72271	Glutamic acid decarbox	4.47e-01
39	76	51.7	20	1 W18846	65 kD glutamic acid de	9.58e-01
40	76	51.7	20	1 W01797	Human 65 kD glutamine	9.58e-01
41	68	46.3	14	1 R76557	Peptide derived from h	7.02e+00
42	68	46.3	14	1 W18865	65 kD glutamic acid de	7.02e+00
43	68	46.3	15	1 W12405	GAD65 residues 177-191	7.02e+00
44	65	44.2	919	1 R84337	Arabidopsis thaliana a	1.46e+01
45	65	44.2	927	1 R85598	Arabidopsis thaliana a	1.46e+01

## ALIGNMENTS

RESULT 1  
 AC W01796: 1  
 DE 15-OCT-1997 (first entry)  
 KW Human 65 kD glutamine decarboxylase peptide.  
 KW Human; glutamine decarboxylase; GAD; diagnosis; predisposition;  
 KW tumour; immunological; disease; autoimmune; diabetes; reagent;  
 KW determination; T cell; subpopulation; medicament; treatment;  
 KW prevention; production; antigen; immunogen; tolerogen; isolation;  
 KW reinjection; inactivation.  
 OS Homo sapiens.  
 PN DE19525784-A.  
 PD 16-JAN-1997.  
 PE 14-JUL-1995; DE-025784.  
 PR 14-JUL-1995; DE-025784.  
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.  
 PI Albert W, Bolhard C, Endl J, Jung G, Schendel D;  
 PI Stahl P, Van Endert P;  
 DR WPI: 97-078452/08.  
 PT Glutamine decarboxylase peptide(s) - for diagnosis and therapy of  
 PT diabetes, etc. 12; 15pp; German.  
 PS Claim 1; Page 12; 15pp; German.  
 CC The present peptide is a fragment of the human 65 kD glutamine  
 CC decarboxylase (GAD), which can be used to diagnose, or diagnose a  
 CC predisposition to, a tumour or immunological disease, preferably an  
 CC autoimmune disease, especially diabetes. It can also be used as a  
 CC reagent to determine specific T cell subpopulations, in medicaments  
 CC to treat or prevent immunological diseases, preferably autoimmune  
 CC diseases, especially diabetes, to produce antigens, especially  
 CC immunogens or tolerogens and to isolate specific T cell  
 CC subpopulations, which can be used to produce antigens or for  
 CC reinjection, optionally after inactivation.  
 SO Sequence 20 AA.

Query Match 100.0%; Score 147; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 TLKYAIKTHPRYFNQLSG 20  
 QY 1 TLKYAIKTHPRYFNQLSG 20

RESULT 2  
 ID W18845 standard; peptide; 20 AA.  
 AC W18845; 1998 (first entry)  
 DT 05-JAN-1998

DF 55 kD glutamic acid decarboxylase peptide fragment IV.  
KW GAD, 65 kD; human; glutamic acid decarboxylase; autoreactive; diagnosis;  
KW insulin-dependent diabetes mellitus; IDDM; cell-mediated disease;  
KW predisposition; autoimmune; tumour; rheumatoid arthritis;  
KW multiple sclerosis.  
OS Synthetic.  
PN DEL9526561-A1.  
PD 23-JAN-1997.  
PF 20-JUL-1995; 026561.  
PR 20-JUL-1995; DE-026561.  
PI (BOEF)-BOEHRINGER/MANNHEIM GMBH.  
PI Donie F, Endl J, Ganz M, Jung G, Kientsch-engel R;  
PI Pozzilli P, Stahl P;  
DR WPI: 97-088254/09.  
PT Skin test for diagnosis of cell-mediated diseases, esp. diabetes -  
PT Involving intradermal admin. of auto-reactive substances  
PS Claim 11; Page 9; 12pp; German.  
CC W18842-70 are peptide fragments of the 65 kD human glutamic acid  
CC decarboxylase (GAD). The fragments are autoreactive substances used for  
CC diagnosis of insulin-dependent diabetes mellitus (IDDM). The diagnosis is  
CC determined by using a claimed method for diagnosis of cell-mediated  
CC diseases or a predisposition to cell-mediated diseases, which is effected  
CC by administering an autoreactive substance intradermally and establishing  
CC the diagnosis on the basis of the occurrence or lack of a positive  
CC reaction at the site of administration. The method is used for diagnosis  
CC of autoimmune and tumour diseases, preferably T-cell-mediated diseases  
CC such as rheumatoid arthritis, multiple sclerosis and especially IDDM.  
SQ Sequence 20 AA;  
  
Query Match 100.0%; Score 147; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 1 TLKXAIKTHPRYNOLSTG 20  
1 TLKXAIKTHPRYNOLSTG 20  
|||||  
  
QY 1 TLKXAIKTHPRYNOLSTG 20  
1 TLKXAIKTHPRYNOLSTG 20  
|||||  
  
RESULT 3  
ID R23645 standard; Protein; 503 AA.  
AC R23645;  
DT 02-NOV-1992 (first entry)  
DE Human GAD65 gene product.  
KW Glutamic acid decarboxylase; IDDM; stiff man syndrome;  
KW autoantibodies.  
OS Homo sapiens.  
PN WO9205446-A.  
PD 02-APR-1992.  
PF 23-SEP-1991; 006872.  
PR 21-SEP-1990; US-586536.  
PA (REGC) UNIV CALIFORNIA.  
PA (REGC) UNIV CALIFORNIA.  
PI Erlanger MG, Kaufman DL, Tobin AJ;  
DR WPI: 92-150489/18.  
DR N-PSDB: 024184.  
PT Novel cDNA encoding GAD65 polypeptide - used to produce GAD65 for  
PT therapeutic and diagnostic application in insulin-dependent  
PT diabetes mellitus patients  
PS Disclosure: Fig 3; 53pp; English.  
CC The sequence given is a glutamic acid decarboxylase (GAD65). GAD65  
CC can be used for the diagnosis and therapy of patients with autoimmune  
CC diseases, esp. insulin-dependant diabetes mellitus (IDDM) and "stiff  
CC man" syndrome. It is possible to use either the entire GAD65 protein  
CC or polypeptide fragments of it for the immunological detection of  
CC autoantibodies to GAD65 which are indicative of IDDM and other auto-  
CC immune diseases. The production of this sequence by recombinant DNA  
CC technology allows large scale production of eukaryotic GAD65 in its  
CC native form without the need for separation from other proteinaceous  
CC prods.  
SQ Sequence 503 AA;  
  
Query Match 100.0%; Score 147; DB 1; Length 503;

Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 166 TLKXAIKTHPRYNOLSTG 185  
1 TLKXAIKTHPRYNOLSTG 185  
|||||  
  
QY 1 TLKXAIKTHPRYNOLSTG 20  
1 TLKXAIKTHPRYNOLSTG 20  
|||||  
  
RESULT 4  
ID R59520 standard; protein; 540 AA.  
AC R59520;  
DT 09-NOV-1994 (first entry);  
DE GAD65 1-45 N-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Narnchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 540 AA;  
  
Query Match 100.0%; Score 147; DB 1; Length 540;  
Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 121 TLKXAIKTHPRYNOLSTG 140  
1 TLKXAIKTHPRYNOLSTG 140  
|||||  
  
QY 1 TLKXAIKTHPRYNOLSTG 20  
1 TLKXAIKTHPRYNOLSTG 20  
|||||  
  
RESULT 5  
ID R59521 standard; protein; 540 AA.  
AC R59521;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-45 N-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KW stiff man syndrome; autoantibody; mutagenesis.  
OS Rattus sp.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC) UNIV CALIFORNIA.  
PI Baekkeskov S, Kim J, Narnchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1; 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 540 AA;  
  
Query Match 100.0%; Score 147; DB 1; Length 540;  
Best Local Similarity 100.0%; Pred. No. 3.73e-09;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 TLKAIKTGHPRYFNOLSTG 140  
|||||  
QY 1 TLKAIKTGHPRYFNOLSTG 20

RESULT 6  
ID R59525 standard; protein: 544 AA.  
AC R59525;  
DT 09-NOV-1994 (first entry)  
DE GAD65 545-585 C-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KM stiff man syndrome; autoantibody; mutagenesis.  
OS Rattus sp.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC ) UNIV CALIFORNIA.  
PI Beekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1: 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. The C-terminally deleted mutants given in R59524-25  
CC are able to recognize IDDM autoantibodies having the specificity  
CC of MICA4/MICA6, but not those having the specificity of MICA1/MICA3  
CC or MICA2. These mutants also have some N-terminal modifications  
CC to improve solubility.  
SQ Sequence 544 AA;

Query Match 100.0%; Score 147; DB 1; Length 544;  
Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTGHPRYFNOLSTG 185  
|||||  
QY 1 TLKAIKTGHPRYFNOLSTG 20

RESULT 7  
ID R59524 standard; protein: 544 AA.  
AC R59524;  
DT 09-NOV-1994 (first entry)  
DE GAD65 545-585 C-terminal-deleted mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KM stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC ) UNIV CALIFORNIA.  
PI Beekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1: 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. The C-terminally deleted mutants given in R59524-25  
CC are able to recognize IDDM autoantibodies having the specificity  
CC of MICA4/MICA6, but not those having the specificity of MICA1/MICA3  
CC or MICA2. These mutants also have some N-terminal modifications  
CC to improve solubility.  
SQ Sequence 544 AA;

Query Match 100.0%; Score 147; DB 1; Length 544;  
Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTGHPRYFNOLSTG 185  
|||||  
QY 1 TLKAIKTGHPRYFNOLSTG 20

RESULT 8  
ID R59518 standard; protein: 554 AA.  
AC R59518;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-31 deleted; C45A mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KM stiff man syndrome; autoantibody; mutagenesis.  
OS Homo sapiens.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC ) UNIV CALIFORNIA.  
PI Beekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1: 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 554 AA;

Query Match 100.0%; Score 147; DB 1; Length 554;  
Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 135 TLKAIKTGHPRYFNOLSTG 154  
|||||  
QY 1 TLKAIKTGHPRYFNOLSTG 20

RESULT 9  
ID R59519 standard; protein: 554 AA.  
AC R59519;  
DT 09-NOV-1994 (first entry)  
DE GAD65 1-31 deleted; C45A mutant.  
KW GAD65; glutamate-decarboxylase; diabetes mellitus;  
KM stiff man syndrome; autoantibody; mutagenesis.  
OS Rattus sp.  
PN WO9412529-A.  
PD 09-JUN-1994.  
PF 02-DEC-1993; U11705.  
PR 03-DEC-1992; US-984935.  
PA (REGC ) UNIV CALIFORNIA.  
PI Beekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
DR WPI: 94-200193/24.  
PT New soluble fragments of glutamic acid decarboxylase protein -  
PT used for the diagnosis and treatment of insulin dependent  
PT diabetes mellitus and stiff man syndrome.  
PS Disclosure: Fig. 1: 73pp; English.  
CC The amino acid sequences of human GAD65 (R59516) and rat GAD65  
CC (R59517) were determined. New soluble fragments of GAD65  
CC (R59518-25) were prepared by deletion/substitution  
CC mutagenesis. These fragments are free of N-terminal amino acids  
CC that limit solubility. Different fragments contain epitopes for  
CC different classes of GAD65 autoantibodies.  
SQ Sequence 554 AA;

Query Match 100.0%; Score 147; DB 1; Length 554;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 135 TLKYAIKTGHPRYFNOLSTG 154  
 |||||||  
 QY 1 TLKYAIKTGHPRYFNOLSTG 20

RESULT 10  
 ID W34520 standard; protein; 584 AA.  
 AC W34520:  
 DT 24-MAR-1998 (first entry)  
 DE Rat GAD65 protein.  
 KW GAD65; glutamic acid decarboxylase protein; rat; soluble fragment;  
 autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
 stiff man syndrome; therapy.  
 OS Rattus sp.  
 PN US5691448-A.  
 PD 25-NOV-1997.  
 PF 02-DEC-1993; 161290.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PA (BAEK/) BAEKESKOV S.  
 PA (KIMJ/) KIM J.  
 PA (NAMC/) NAMCHUK M.  
 PA (RICH/) RICHTER W.  
 PA (SHIY/) SHI Y.  
 PI Baekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 98-01711/02.  
 PT Soluble fragments of glutamic acid decarboxylase GAD65 - used to  
 distinguish between insulin-dependent diabetes mellitus and  
 stiff man syndrome  
 PS This sequence represents the rat glutamic acid decarboxylase protein  
 disclosure; column 31-34: 30pp; English.  
 CC This sequence relates to soluble fragments of a GAD65 protein that  
 are specifically reactive with a GAD65 autoantibody (AAb), where the  
 fragment is at least 98% pure and the AAb binds to a conformational  
 epitope of the fragment. The soluble GAD65 fragments can be used to  
 distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff  
 man syndrome. They can be used for diagnosis and treatment of IDDM  
 CC and stiff man syndrome. The fragments can distinguish different temporal  
 stages in the progression of IDDM.  
 CC Sequence 584 AA;  
 SQ

Query Match 100.0%; Score 147; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKYAIKTGHPRYFNOLSTG 185  
 |||||||  
 QY 1 TLKYAIKTGHPRYFNOLSTG 20

RESULT 11  
 ID W86018 standard; protein; 584 AA.  
 AC W86018:  
 DT 22-FEB-1999 (first entry)  
 DE Rat GAD65 protein sequence.  
 KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
 insulin-dependent diabetes mellitus; stiff man syndrome.  
 OS Rattus sp.  
 PN US5849506-A.  
 PD 15-DEC-1998.  
 PF 25-MAY-1995; 450755.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PR 25-MAY-1995; US-450755.  
 PA (RECC) UNIV CALIFORNIA.  
 PI Baekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 99-069720/06.  
 PT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
 diabetes and stiff man syndrome

PS Examples; Fig 1; 31pp; English.  
 CC This represents a human GAD65 protein sequence. The invention provides  
 CC soluble fragments of GAD65 that are specifically reactive with at least  
 CC one class of GAD65 autoantibody. The fragments are substantially free of  
 CC N-terminal amino acids that would otherwise limit solubility. Different  
 CC fragments contain different epitopes for different classes of GAD65  
 CC autoantibodies. These fragments are used in the methods of the invention  
 CC for detection of GAD65 autoantibodies. The methods are used for  
 CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and  
 CC stiff man syndrome.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 147; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKYAIKTGHPRYFNOLSTG 185  
 |||||||  
 QY 1 TLKYAIKTGHPRYFNOLSTG 20

RESULT 12  
 ID W86017 standard; protein; 584 AA.  
 AC W86017:  
 DT 22-FEB-1999 (first entry)  
 DE Human GAD65 protein sequence.  
 KW GAD65; autoantibody; soluble; detection; diagnosis; monitor; IDDM;  
 insulin-dependent diabetes mellitus; stiff man syndrome.  
 OS Homo sapiens.  
 PN US5849506-A.  
 PD 15-DEC-1998.  
 PF 25-MAY-1995; 450755.  
 PR 02-DEC-1993; US-161290.  
 PR 03-DEC-1992; US-984935.  
 PR 25-MAY-1995; US-450755.  
 PA (RECC) UNIV CALIFORNIA.  
 PI Baekeskov S, Kim J, Namchuk M, Richter W, Shi Y;  
 DR WPI: 99-069720/06.  
 PT Immunoassay for GAD65 auto-antibodies - used for diagnosis of  
 PT diabetes and stiff man syndrome  
 PS Examples; Fig 1; 31pp; English.  
 CC This represents a human GAD65 protein sequence. The invention provides  
 CC soluble fragments of GAD65 that are specifically reactive with at least  
 CC one class of GAD65 autoantibody. The fragments are substantially free of  
 CC N-terminal amino acids that would otherwise limit solubility. Different  
 CC fragments contain different epitopes for different classes of GAD65  
 CC autoantibodies. These fragments are used in the methods of the invention  
 CC for detection of GAD65 autoantibodies. The methods are used for  
 CC diagnosing or monitoring insulin-dependent diabetes mellitus (IDDM) and  
 CC stiff man syndrome.  
 SQ Sequence 584 AA;

Query Match 100.0%; Score 147; DB 1; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 3.73e-09;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKYAIKTGHPRYFNOLSTG 185  
 |||||||  
 QY 1 TLKYAIKTGHPRYFNOLSTG 20

RESULT 13  
 ID W34519 standard; protein; 584 AA.  
 AC W34519:  
 DT 24-MAR-1998 (first entry)  
 DE Human GAD65 protein.  
 KW GAD65; glutamic acid decarboxylase protein; human; soluble fragment;  
 autoantibody; insulin-dependent diabetes mellitus; IDDM; diagnosis;  
 stiff man syndrome; therapy.  
 OS Homo sapiens.  
 PN US5691448-A.  
 PD 25-NOV-1997.  
 PF 02-DEC-1993; 161290.



```

PR 02-DEC-1993: US-161290.
PR 03-DEC-1992: US-984935.
PA (BAEK/) BAEKESKOV S.
PA (KIMJ/) KIM J.
PA (NAMC/) NAMCHUK M.
PA (RICH/) RICHTER W.
PA (SHIY/) SHI Y.
PI Baekeskov S, Kim J, Namchuk M, Richter W, Shi Y;
PI WPI: 98-017711/02.
PT Soluble fragments of glutamic acid decarboxylase GAD65 - used to
PT distinguish between insulin-dependent diabetes mellitus and
PT stiff-man syndrome
PS Disclosure: column 27-30; 30pp; English.
CC This sequence represents the human glutamic acid decarboxylase protein
CC GAD65. The invention relates to soluble fragments of a GAD65 protein that
CC are specifically reactive with a GAD65 autoantibody (AAb), where the
CC fragment is at least 9% pure and the AAb binds to a conformational
CC epitope of the fragment. The soluble GAD65 fragments can be used to
CC distinguish between insulin-dependent diabetes mellitus (IDDM) and stiff
CC man syndrome. They can also be used for diagnosis and treatment of IDDM
CC and stiff man syndrome. The fragments can distinguish different temporal
CC stages in the progression of IDDM.
SQ Sequence 584 AA;

Query Match 100.0%; Score 147; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 3.73e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTGHPRYFNOLSTG 185
OY 1 TLKAIKTGHPRYFNOLSTG 20
|||||

RESULT 14
ID R79105 standard: Protein: 585 AA.
AC R79105;
DE 13-NOV-1995 (first entry)
DE Human glutamic acid decarboxylase (GAD65).
KM Rat glutamic acid decarboxylase; GAD65; autoimmune disorders;
KM Insulin-dependent diabetes mellitus; stiff man disease.
OS Homo sapiens.
PN W09507992-A.
PD 23-MAR-1995.
PE 24-AUG-1994; U09478.
PR 17-SEP-1993; US-123859.
PA (REGC ) UNIV CALIFORNIA.
PI Clare-Salzler MJ, Erlander MG, Kaufman DL, Tobin AJ;
PI WPI: 95-131360/17.
DR N-PSDB; Q86482.
PT New polypeptide fragments of glutamic acid decarboxylase - for
PT diagnosis and treatment of autoimmune disease; esp. insulin
PT dependent diabetes; also related nucleic acid, vectors,
PT antibodies, hybridoma(s) etc.
PS Example 1; Fig 3; 10pp; English.
CC Q86481 and Q86482 encode R71733 and R79105, rat and human glutamic
CC acid decarboxylase (GAD65) respectively, from which the GAD65
CC fragments described in R72261-R72298 were derived. These fragments
CC can be used to detect autoantibodies against GAD, e.g. to diagnose
CC and treat GAD-related autoimmune disorders, such as insulin
CC dependant diabetes mellitus or stiff man disease.
SQ Sequence 585 AA;

Query Match 100.0%; Score 147; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.73e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTGHPRYFNOLSTG 185
OY 1 TLKAIKTGHPRYFNOLSTG 20
|||||

RESULT 15
ID W14915 standard: Protein: 585 AA.

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AC W14915;
DT 10-JUL-1997 (first entry)
DE Modified glutamic acid decarboxylase (K396R).
DE Glutamic acid decarboxylase; GAD; autoimmune disease; therapy;
KM Insulin-dependent diabetes mellitus; vaccine;
KW enzyme engineering; protein engineering.
OS Synthetic.
PN W09712034-A1.
PD 03-APR-1997.
PE 27-SEP-1996; SE1210.
PR 28-SEP-1995; SF-003379.
PA (SYNE-) SYNECTICS BIOTECHNOLOGY AB.
PI Essen-Moeller A, Falorni A, Lermarck A, Robertson J;
PI WPI: 97-212895/19.
DR N-PSDB; T64560.
PT Modified glutamic acid decarboxylase for autoimmune disease
PT treatment - has immunoreactivity of unmodified GAD65 but decreased
PT enzyme activity, esp. useful for insulin-dependent diabetes mellitus
PT treatment
PS Claim 3; Page 13-15; 24pp; English.
CC A modified human glutamic acid decarboxylase (GAD) (W14915) has the
CC native lysine residue at amino acid position 396 replaced by
CC arginine. It is obtd. by site-directed mutagenesis (see also
CC T64561) of native human GAD65 cDNA and expression of the mutant DNA
CC (T64560) in transformed host cells. Lys-396 is critical for enzyme
CC activity. By replacing it with an amino acid incapable of Schiff
CC base formation, immunoreactivity is maintained but enzyme activity
CC is reduced or lost, so minimising the risk of toxicity. The
CC modified GAD can be used to treat and/or prevent autoimmune
CC disorders such as insulin-dependent diabetes mellitus (IDDM) and
CC other diseases, e.g. neurological diseases, esp. in individuals
CC having a genetic predisposition for IDDM or with an increased
CC antibody titre against GAD.
SQ Sequence 585 AA;

Query Match 100.0%; Score 147; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 3.73e-09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKTGHPRYFNOLSTG 185
OY 1 TLKAIKTGHPRYFNOLSTG 20
|||||

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Kauffman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin
A.J.
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa
GAD, are each encoded by a single gene.
#cross-references MIM:92196068
#accession A41935
##molecule_type mRNA
##residues 1-585 ##label BU1
##cross-references GB:M1882; NID:g182933; PIDN:AAA62367.1; PID:g182934
##experimental_source Brain
##note Sequence extracted from NCBI backbone (NCBIP:88007)
REFERENCE
#authors Karlisen, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.;
Disteche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.;
Grant, F.J.; Foster, D.; Iermak, A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341
#title Cloning and primary structure of a human islet isoform of
glutamic acid decarboxylase from chromosome 10.
#cross-references MIM:92020848
#accession A41292
##molecule_type mRNA
##residues 1-585 ##label KAR
##cross-references GB:M74826; NID:g182931; PIDN:AAA58491.1; PID:g182932
##experimental_source pancreatic islet
REFERENCE
#authors Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel,
B.; Northmann, W.
#journal Eur. J. Biochem. (1993) 212:597-603
#title Characterization of a linear epitope within the human
pancreatic 64-kDa glutamic acid decarboxylase and its
autoimmune recognition by sera from insulin-dependent
diabetes mellitus patients.
#cross-references MIM:93185681
#accession S30058
##molecule_type mRNA
##residues 6-585 ##label MAU
##cross-references EMBL:X69936
##experimental_source pancreatic islet
REFERENCE
#authors Bu, D.F.; Tobin, A.J.
#journal Genomics (1994) 21:222-228
#title The exon-intron organization of the genes (GAD1 and GAD2)
encoding two human glutamate decarboxylases (GAD-67 and
GAD-65) suggests that they derive from a common ancestral
GAD.
#cross-references MIM:94375018
#contents annotation: intron-exon boundaries
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
it has several isoforms, each encoded by a separate gene. GAD has
also been implicated as an autoantigen in autoimmune disease
stiff-man syndrome and insulin-dependent diabetes mellitus.
GENETICS
#gene GDB:GAD2
##cross-references GDB:128595; OMIM:138275
#map_position 10p11.23-10p11.23
CLASSIFICATION #superfamily human glutamate decarboxylase
carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
phosphate
FEATURE
#binding_site pyridoxal phosphate (lys) (covalent)
#status predicted
396
SUMMARY #length 585 #molecular-weight 65411 #checksum 4799
Query Match 100.0%; Score 147; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1,16e-18;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 166 TLKAIKTHPRYFNOLSTG 185
|||||
1 TLKAIKTHPRYFNOLSTG 20

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RESULT      3
ENTRY      3S8533 #type complete
TITLE      glutamate decarboxylase (EC 4.1.1.15) 2 - mouse
ALTERNATE_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase
ORGANISM   #format_name Mus musculus #common_name house mouse
DATE       20-May-1994 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999

ACCESSIONS 3S8533
REFERENCE   3S8533
#authors   Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.
#journal   Blochim. Biophys. Acta (1993) 1216:157-160
#title     Cloning and sequence analysis of a murine cDNA encoding glutamate decarboxylase (GAD65).
#cross-references MIMD:94032481
#accession 3S8533

##status preliminary
##molecule_type mRNA
##residues 1-585 #label LEE
##cross-references GB:LI16980; NID:G413867; PIDN:AAA93049.1; PID:G413868
COMMENT    This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS     carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxaxaphosphate

FEATURE
396
#binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
SUMMARY      #length 585 #molecular_weight 65224 #checksum 7599

Query Match 100.0%; Score 147; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1,15e-18;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKAIKIGHPRYNOLSTG 185
Oy 1 TLKAIKIGHPRYNOLSTG 20
|||||
|||||

RESULT      4
ENTRY      JH0423 #type complete
TITLE      glutamate decarboxylase (EC 4.1.1.15) 2 - rat
ALTERNATE_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase
ORGANISM   #format_name Rattus norvegicus #common_name Norway rat
DATE       31-Mar-1992 #sequence_revision 23-Mar-1995 #text_change 18-Jun-1999

ACCESSIONS JH0423; A60888
REFERENCE   JH0423
#authors   Erlander, M.G.; Tillakaratne, N.J.K.; Feldblum, S.; Patel, N.; Tobin, A.J.
#journal   Neuron (1991) 7:91-100
#title     Two genes encode distinct glutamate decarboxylases.
#cross-references MIMD:91299343
#accession JH0423

##molecule_type mRNA
##residues 1-585 #label ERL
##cross-references GB:M72422; NID:G204225; PIDN:AAA63488.1; PID:G204226
##experimental_source brain
#note      the authors translated the codon GAT for residue 86 as His, TCA for residue 198 as Ala, and CAG for residue 428 as Trp

REFERENCE   A60888
#authors   Chang, Y.C.; Gottlieb, D.I.
#journal   J. Neurosci. (1988) 8:2123-2130
#title     Characterization of the proteins purified with monoclonal antibodies to glutamic acid decarboxylase.
#cross-references MIMD:88258610
#accession A60888

##status preliminary
##molecule_type protein
#residues 191-194, 'X', 196-203, 'XX', 206-219, 'X', 225-234, 'X', 236-247, 'X', 249-266, 'X', 524-537, 539-543, 'V', 547-549,

```

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid. It has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase

KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 396 #binding-site pyridoxal phosphate (Lys) (covalent) #status predicted

SUMMARY #length 585 #molecular-weight 65402 #checksum 7756

Query Match 100.0%: Score 147; DB 1; Length 585; Best Local Similarity 100.0%: Pred. No. 1.16e-18; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 166 TLKYAIKTGHPRFNQSTG 185  
|||||

QY 1 TLKYAIKTGHPRFNQSTG 20

RESULT 5

ENTRY 159173 #type complete

TITLE glutamate decarboxylase - rat

ALTERNATE\_NAMES #formal\_name Rattus norvegicus #common\_name Norway rat

ORGANISM 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change

DATE 22-Jun-1999

ACCESSIONS 159173

REFERENCE 159173 Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775

#authors #journal Developmentally regulated expression of an exon containing a stop codon in the gene for glutamic acid decarboxylase.

#title #cross-references MUID:91062362

#accession 159173

#status preliminary; translated from GB/EMBL/DBJ

#molecule\_type mRNA

#residues 1-223 ##label RES

CLASSIFICATION #cross-references GB:M38350; NID:9204231; PIDN:AAA1185.1; PID:9204232

SUMMARY #superfamily human glutamate decarboxylase

#length 223 #molecular-weight 25069 #checksum 1388

Query Match 91.2%: Score 134; DB 2; Length 223; Best Local Similarity 80.0%: Pred. No. 1.62e-15; Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGRTGHPRFNQLSTG 193  
|||||

QY 1 TLKYAIKTGHPRFNQSTG 20

RESULT 6

ENTRY 561534 #type complete

TITLE glutamate decarboxylase (EC 4.1.1.15) 62k isoform - mouse

ALTERNATE\_NAMES glutamic acid decarboxylase

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change

ACCESSIONS 561534

REFERENCE 561534 Katarova, Z.; Szabo, G.; Mugnaini, E.; Greenspan, R.J. Eur. J. Neurosci. (1990) 2:190-202

#authors #journal Molecular identification of the 62 kd form of glutamic acid decarboxylase from the mouse.

#title #accession 561534

#molecule\_type mRNA

#residues 1-585 ##label KAT

CLASSIFICATION #cross-references EMBL:249976

KEYWORDS #experimental\_source brain

REFERENCE 561533 Szabo, G. submitted to the EMBL Data Library, June 1995

#authors #submission

#accession 561533

#molecule\_type mRNA

#residues 1-534, 'YOPQGDKNFFRMVSNPASQSDIDFTEETIERLGQDL' ##label SZA

#cross-references EMBL:249976; NID:9886686; PIDN:CAA90277.1; PID:9886687

#experimental\_source brain

#note the differences at the carboxyl end are due to a frameshift error

CLASSIFICATION #superfamily human glutamate decarboxylase

KEYWORDS carbon-carbon lyase; carboxy-lyase

SUMMARY #length 585 #molecular-weight 65381 #checksum 5716

Query Match 91.2%: Score 134; DB 2; Length 585; Best Local Similarity 80.0%: Pred. No. 1.62e-15; Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGRTGHPRFNQLSTG 193  
|||||

QY 1 TLKYAIKTGHPRFNQSTG 20

RESULT 7

ENTRY A41367 #type complete

TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - rat

ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase

ORGANISM #formal\_name Rattus norvegicus #common\_name Norway rat

DATE 12-Jun-1992 #sequence\_revision 23-Mar-1995 #text\_change

ACCESSIONS A41367; A43756; JH0195

REFERENCE A41367 Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.; Dyrberg, T.; Madsen, O.D. Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758

#authors #journal Cloning, characterization, and autoimmune recognition of rat islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.

#title #cross-references MUID:92020930

#accession A41367

#status preliminary

#molecule\_type mRNA

#residues 1-593 ##label MIC

REFERENCE A43756 Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I. Brain Res. Mol. Brain Res. (1990) 8:193-198

#authors #journal Characterization of a cDNA coding for rat glutamic acid decarboxylase.

#title #cross-references MUID:91014554

#accession A43756

#status preliminary

#molecule\_type mRNA

#residues 1-593 ##label WYB

#cross-references GB:X57573; NID:956183; PIDN:CAA40801.1; PID:956184

#note the authors translated the codon TGT for residue 412 as Ser and TCT for residue 413 as Cys

REFERENCE JH0195 Julien, J.F.; Samama, P.; Mallet, J. J. Neurochem. (1990) 54:703-705

#authors #journal Rat brain glutamic acid decarboxylase sequence deduced from a cloned cDNA.

#title #accession JH0195

#molecule\_type mRNA

#residues 1-102, 'V', 104-283, 'S', 285-286, 'AD', 289-343, 'EA', 346, 'I', 348-351, 'LE', 354-379, 'R', 381-593 ##label JUL

CLASSIFICATION #cross-references GB:X57572; NID:956185; PIDN:CAA40800.1; PID:956186

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid. It has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase

KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE

404 #binding\_site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 593 #molecular-weight 66640 #checksum 3971

Query Match 91.2%: Score 134; DB 1; Length 593;  
Best Local Similarity 80.0%: Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRGTHPRFFNOLSTG 193  
1 TLKYAIRKTHPRFFNOLSTG 20

RESULT 8  
ENTRY S48135 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORANISM #formal\_name Homo sapiens #common\_name man  
DATE 14-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 07-May-1999

ACCESSIONS S48135  
REFERENCE S48135  
#authors Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.; Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.  
#journal Ann. Hum. Genet. (1992) 56:255-265  
#title Nucleotide sequence and chromosomal assignment of a cDNA encoding the large isoform of human glutamate decarboxylase.  
#cross-references M01D:93080286  
#accession S48135  
#molecule\_type mRNA  
#residues 1-593 #label KEL

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS #carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66952 #checksum 4836

Query Match 91.2%: Score 134; DB 2; Length 593;  
Best Local Similarity 80.0%: Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRGTHPRFFNOLSTG 193  
1 TLKYAIRKTHPRFFNOLSTG 20

RESULT 9  
ENTRY S51776 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORANISM #formal\_name Homo sapiens #common\_name man  
DATE 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Feb-1997

ACCESSIONS S51776  
REFERENCE S51776  
#authors Johnstone, A.  
#submission submitted to the EMBL Data Library, May 1993  
#accession S51776  
#status preliminary  
#molecule\_type mRNA  
#residues 1-593 #label JOH  
#cross-references EMBL:223750  
#note this is an unpublished revision to the sequence from reference S48135

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS #carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66946 #checksum 4842

Query Match 91.2%: Score 134; DB 2; Length 593;  
Best Local Similarity 80.0%: Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRGTHPRFFNOLSTG 193  
1 TLKYAIRKTHPRFFNOLSTG 20

RESULT 10  
ENTRY B41935 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORANISM #formal\_name Homo sapiens #common\_name man  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS B41935; JH0805; A61406; P00157; P00158; B41367;  
B41935; JH0805; A54778  
A36463; A54778

REFERENCE B41935  
#authors Bu, D.F.; Erlander, M.G.; Hiltz, B.C.; Tiliakaratne, N.J.K.; Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J.  
Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#journal Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.  
#cross-references M01D:92196068  
#accession B41935  
#molecule\_type mRNA  
#residues 1-594 #label BU1  
#cross-references GB:81883; NID:g182935; PIDN:AAA62368.1; PID:g182936  
#experimental\_source pancreatic islet  
#note sequence extracted from NCBI backbone (NCBIP:88006)

REFERENCE JH0805  
#authors Kawasaki, E.; Moriwaki, R.; Watanabe, M.; Saitoh, K.; Charles Brunicaudi, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.; Akazawa, S.; Miyamoto, T.; Nagataki, S.  
Biochem. Biophys. Res. Commun. (1993) 192:1353-1359  
#journal Cloning and expression of large isoform of glutamic acid decarboxylase from human pancreatic islet.  
#cross-references M01D:93282845  
#accession JH0805  
#molecule\_type mRNA  
#residues 1-17, 'N', '19-30', 'N', '32-67', 'K', '69-115', 'L', '117-154', 'T', '156-301', 'C', '303-476', 'G', '478-491', 'G', '493-594' #label KAW

#cross-references GB:561898; NID:g385310; PIDN:AAB26938.1; PID:g385311  
#experimental\_source pancreatic islet  
REFERENCE JH0806  
#authors Yamashita, K.; Cram, D.S.; Harrison, L.C.  
Biochem. Biophys. Res. Commun. (1993) 192:1347-1352  
#journal Molecular cloning of full-length glutamic acid decarboxylase 67 from human pancreas and islets.  
#cross-references M01D:93282844  
#accession JH0806  
#molecule\_type mRNA  
#residues 1-67, 'K', '69-435', 'L', '437-511', 'S', '513-594' #label YAM

#cross-references GB:561897; NID:g385450; PIDN:AAB26937.1; PID:g385451  
#experimental\_source pancreatic islet  
REFERENCE A61406  
#authors Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.  
Lancet (1991) 338:1468-1469  
#journal Cloning of large isoform of human brain glutamic acid decarboxylase.  
#cross-references M01D:92065769  
#accession A61406  
#molecule\_type mRNA  
#residues 62-67, 'K', '69-205', 'N', '207-564', 'L', '566-594' #label KEL

#experimental\_source brain  
REFERENCE P00157  
#authors Cram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C.  
Biochem. Biophys. Res. Commun. (1991) 176:1239-1244  
#journal Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets.  
#cross-references M01D:91248209  
#accession P00157  
#molecule\_type mRNA  
#residues 218-463 #label CRI  
#cross-references GB:M70434  
#experimental\_source brain  
#accession P00158

##molecule\_type mRNA  
##residues 218-234,'K',236-240,'N',242-288,'H',290-323,'L',325-329,  
D',331-338,'L',340-390,'S',392-397 ##label CR2  
##cross-references GB:M70435; NID:g182941; PID:g182942  
##experimental\_source pancreatic islet  
REFERENCE A41367  
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;  
Dyrberg, T.; Madsen, O.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
#title Cloning, characterization, and autoimmune recognition of rat  
islet glutamic acid decarboxylase in insulin-dependent  
diabetes mellitus.  
##cross-references MUID:92020930  
#accession B41367  
##molecule\_type mRNA  
##residues 317-482,'R',484-594 ##label MIC  
REFERENCE A36463  
#authors Persson, H.; Pelto-Huikko, M.; Metsis, M.; Soeder, O.; Brene,  
S.; Skog, S.; Hoekfelt, T.; Ritzén, E.M.  
#journal Mol. Cell. Biol. (1990) 10:4701-4711  
#title Expression of the neurotransmitter-synthesizing enzyme  
glutamic acid decarboxylase in male germ cells.  
##cross-references MUID:90355986  
#accession A36463  
##molecule\_type mRNA  
##residues 527-594 ##label PER  
##cross-references GB:M55574; NID:g182929; PIDN:AA2938.1; PID:g182930  
REFERENCE A54778  
#authors Bu, D.F.; Tobin, A.J.  
#journal Genomics (1994) 21:222-228  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
encoding two human glutamate decarboxylases (GAD-67 and  
GAD-65) suggests that they derive from a common ancestral  
GAD.  
##cross-references MUID:94375018  
#contents annotation: intron-exon organization  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene. GAD has  
also been implicated as an autoantigen in autoimmune disease  
stiff-man syndrome and insulin-dependent diabetes mellitus.  
GENETICS  
#gene GDB:GAD1; GAD  
##cross-references GDB:119244; OMIM:266100  
#map\_position 2q31-2q31  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS alternative splicing; carbon-carbon lyase; carboxy-lyase;  
phosphoprotein; pyridoxal phosphate  
FEATURE 405  
#binding\_site pyridoxal phosphate (lys) (covalent)  
#status predicted  
SUMMARY #length 594 #molecular\_weight 66924 #checksum 6189  
Query Match 91.2%; Score 134; DB 1; Length 594;  
Best Local Similarity 80.0%; Pred. No. 1,62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
DB 1 TLKXKRTGHPREFNOLSTG 20  
LY 175 TLKXKRTGHPREFNOLSTG 194  
||||:||||:||||:||||:  
QY 1 TLKXKRTGHPREFNOLSTG 20  
RESULT 11  
ENTRY JC4065 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 67k chain - pig  
ORGANISM #formal\_name Sus scrofa domestica #common\_name domestic pig  
DATE 30-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change  
22-Jun-1999  
ACCESSIONS JC4065  
REFERENCE JC4064  
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuna, M.  
#journal Gene (1995) 152:257-260  
#title Sequences of two porcine glutamic acid decarboxylases (65-and

67-kDa GAD)  
##cross-references MUID:95137399  
#accession JC4065  
##molecule\_type mRNA  
##residues 1-594 ##label SUZ  
##cross-references DBJ:D31849; NID:9790966; PIDN:BA06636.1;  
PID:dl007208; PID:g790967  
#experimental\_source brain  
COMMENT This enzyme catalyzes the conversion of glutamic acid into  
gamma-amino butyric acid.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
FEATURE 402-405  
#domain DOPA decarboxylase binding #status predicted  
SUMMARY #length 594 #molecular\_weight 66894 #checksum 5491  
Query Match 91.2%; Score 134; DB 2; Length 594;  
Best Local Similarity 80.0%; Pred. No. 1,62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
DB 175 TLKXKRTGHPREFNOLSTG 194  
||||:||||:||||:||||:  
QY 1 TLKXKRTGHPREFNOLSTG 20  
RESULT 12  
ENTRY S51775 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change  
22-Jun-1999  
ACCESSIONS S51775  
REFERENCE S51775  
#authors Johnstone, A.  
#submision submitted to the EMBL Data Library, May 1993  
#accession S51775  
#status preliminary  
##molecule\_type mRNA  
##residues 1-594 ##label JOH  
##cross-references EMBL:222750; NID:g298098; PIDN:CA080435.1;  
PID:g298099  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 594 #molecular\_weight 66973 #checksum 6437  
Query Match 91.2%; Score 134; DB 2; Length 594;  
Best Local Similarity 80.0%; Pred. No. 1,62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
DB 175 TLKXKRTGHPREFNOLSTG 194  
||||:||||:||||:||||:  
QY 1 TLKXKRTGHPREFNOLSTG 20  
RESULT 13  
ENTRY A46758 #type complete  
TITLE glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Felis silvestris catus #common\_name domestic cat  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change  
18-Jun-1999  
ACCESSIONS A46758  
REFERENCE A46758  
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.  
#submision submitted to GenBank, September 1989  
#accession A46758  
##molecule\_type mRNA  
##residues 1-594 ##label KOB  
##cross-references GB:M16629; NID:g163858; PIDN:AAA51430.1; PID:g163859  
REFERENCE A4671  
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.  
#journal J. Neurosci. (1987) 7:2768-2772

#title glutamic acid decarboxylase cDNA: nucleotide sequence  
#cross-references M01D:87310623  
#accession A45671  
#molecule-type mRNA  
#residues 1-558, 'RGTRPTSGSSRRQLHSPITSSRR', #label K02  
#note this sequence has been revised in reference A46758  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS  
#gene GAD1  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS #carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 405  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
#length 594 #molecular-weight 66824 #checksum 5630

SUMMARY  
Query Match 91.2%; Score 134; DB 1; Length 594;  
Best Local Similarity 80.0%; Pred. No. 1.62e-15;  
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 175 TLKYVKTGHPHFNOJLSTG 194  
|||||:|||||:|||||  
QY 1 TLKYAIKTGHPHFNOJLSTG 20

RESULT 14  
ENTRY A30999 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) Cl - fruit fly  
(Drosophila melanogaster)  
ALTERNATE\_NAMES L-glutamate 1-carboxy-lyase  
ORGANISM #formal name Drosophila melanogaster  
DATE 26-Oct-1989 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1998  
JH0192; PS0301; A30999

ACCESSIONS  
REFERENCE Jackson, F.R.; Newby, L.M.; Kulkarni, S.J.  
J. Neurochem. (1990) 54:1068-1078  
#title Drosophila GABAergic systems: sequence and expression of glutamic acid decarboxylase.  
#cross-references M01D:90155291  
#accession JH0192  
#molecule-type mRNA  
#residues 1-510 #label JAC  
#cross-references GB:X76198; NID:g433082; PIDN:CA53791.1; PID:g433083  
#accession PS0301  
#molecule-type mRNA

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS  
#gene FlyBase:Gad1  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS #carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 322  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
#length 510 #molecular-weight 57758 #checksum 3194

SUMMARY  
Query Match 83.7%; Score 123; DB 1; Length 510;  
Best Local Similarity 75.0%; Pred. No. 6.52e-13;  
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 92 TLKYVKTGHPHFNOJLSTG 111  
|||||:|||||:|||||  
QY 1 TLKYAIKTGHPHFNOJLSTG 20

RESULT 15  
ENTRY S71489 #type complete  
TITLE sulfolanine decarboxylase (EC 4.1.1.29) - rat  
ALTERNATE\_NAMES cysteine sulfinatase decarboxylase; cysteine sulfinic acid decarboxylase  
ORGANISM #formal name Rattus norvegicus #common name Norway rat  
DATE 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 22-Jun-1999  
S71489; S78208; S55689; S55690

ACCESSIONS  
REFERENCE  
#authors Raymond, I.; Sergeant, A.; Tappaz, M.  
#journal Biochim. Biophys. Acta (1996) 1307:152-156  
#title Molecular cloning and sequence analysis of the cDNA encoding rat liver cysteine sulfinatase decarboxylase (CSD).  
#cross-references M01D:96283809  
#accession S71489  
#molecule-type mRNA  
#residues 1-493 #label REV  
#cross-references EMBL:X94152; NID:g1263163; PIDN:CA63868.1; PID:e218415; PID:g1263164  
#experimental\_source liver

REFERENCE  
#molecule-type protein  
#residues S55689  
#authors Katsakia, P.J.; Jerkins, A.A.; Goodspeed, D.C.; Steele, R.D.  
#journal Biochim. Biophys. Acta (1995) 1262:79-82  
#title Cloning and characterization of rat cysteine sulfinic acid decarboxylase.  
#cross-references M01D:95290499  
#note the author's name has been corrected in reference S60723  
#accession S55689  
#molecule-type mRNA  
#residues 1-177, 'V', '179-457', 'W', '459', 'PGPTSSDMMWPTPYWSNP', #label KAI  
#cross-references EMBL:M64755; NID:g847652; PIDN:AC42063.1; PID:g847653

REFERENCE  
#accession S55690  
#status preliminary  
#molecule-type protein  
#residues 220-230 #label KAZ  
S60723  
#authors Katsaki, P.J.; Jerkins, A.A.; Goodspeed, D.C.; Steele, R.D.  
#journal Biochim. Biophys. Acta (1995) 1263:179  
#note annotation: erratum  
#note this a correction of the author's name from reference S55689  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS #carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 305  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
#length 493 #molecular-weight 55248 #checksum 7867

SUMMARY  
Query Match 73.5%; Score 108; DB 2; Length 493;  
Best Local Similarity 63.2%; Pred. No. 1.83e-09;  
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 78 IHYSVKTGHPHFNOJLSTG 96  
|||||:|||||:|||||  
QY 2 LKYAIKTGHPHFNOJLSTG 20

Search completed: Tue Mar 7 21:35:34 2000  
Job time : 9 secs.





```

DB      166 TLKYAIKTGHPRYFNOLSTG 185
      |||||||
OY      1 TLKYAIKTGHPRYFNOLSTG 20

RESULT 2
ID      DCE2_PIG      STANDARD:      PRT:      585 AA.
AC      P48321.
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE      (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN      GAD2 OR GAD65.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-BRAIN;
RX      MEDLINE: 95137399.
KA      SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
RT      "Sequences of two porcine glutamic acid decarboxylases (65- and
RT      67-kDa GAD).";
RL      Gene 152:257-260(1995).
CC      -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC      -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC      -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC      TYRDC).
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: D31848; BAA06635.1; -
DR      PROSITE: PS00392; DDC_GAD_HDC_YDC: 1.
DR      PFAM: PF00282; pyridoxal_dec: 1.
KW      Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW      pyridoxal phosphate; Multigene family.
FT      BINDING: 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ      SEQUENCE 585 AA; 65388 MW; F3E9BD88 CRC32;

Query Match      100.0%; Score 147; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.54e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      166 TLKYAIKTGHPRYFNOLSTG 185
      |||||||
OY      1 TLKYAIKTGHPRYFNOLSTG 20

RESULT 3
ID      DCE2_HUMAN      STANDARD:      PRT:      585 AA.
AC      O05329;
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      01-FEB-1996 (Rel. 33, Last annotation update)
DE      GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE      (65 KD GLUTAMIC ACID DECARBOXYLASE).
GN      GAD2 OR GAD65.
OS      Homo sapiens (Human)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC      Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE: 92196068.
KA      BU D.-F., ERLANDER M.G., HITZ B.C., TILAKARATNE N.J., KAUFMAN D.L.,

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RA      WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;
RT      "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are
RT      each encoded by a single gene.";
RL      Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      MEDLINE: 94375018.
KA      BU D.-F., TOBIN A.J.;
RT      "The exon-intron organization of the genes (GAD1 and GAD2) encoding
RT      two human glutamate decarboxylases (GAD67 and GAD65) suggests that
RT      they derive from a common ancestral GAD.";
RL      Genomics 21:222-228(1994).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE-PANCREATIC ISLETS;
RX      MEDLINE: 92020848.
KA      KARLSEN A.E., HAGOPIAN W.A., GRUBIN C.E., DOBE S., DISTECHE C.M.,
RA      ADLER D.A., BARMETER H., MATHEWS S., GRANT F.J., FOSTER D.,
RA      LERMARK A.;
RT      "Cloning and primary structure of a human islet isoform of glutamic
RT      acid decarboxylase from chromosome 10.";
RL      Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).
RN      [4]
RP      SEQUENCE OF 6-585 FROM N.A.
RC      TISSUE-PANCREAS;
RX      MEDLINE: 93185681.
KA      MAUCH L., ABNEY C.C., BERG H., SCHERBAUM W.A., LIEBVOGEL B.,
RA      NORTHEMAN W.;
RT      "Characterization of a linear epitope within the human pancreatic
RT      64-kDa glutamic acid decarboxylase and its autoimmune recognition by
RT      sera from insulin-dependent diabetes mellitus patients.";
RL      Eur. J. Biochem. 212:597-603(1993).
CC      -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC      -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC      -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
CC      DECARBOXYLASE.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: M81882; AAA62367.1; -
DR      EMBL: M74826; AAA58491.1; -
DR      EMBL: X69936; CAA49554.1; ALT_INIT.
DR      EMBL: M70435; AAA52513.1; -
DR      PIR: A41292; A41292.
DR      PIR: P00158; P00158.
DR      MIM: 138275; -
DR      PROSITE: PS00392; DDC_GAD_HDC_YDC: 1.
DR      PFAM: PF00282; pyridoxal_dec: 1.
KW      Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW      pyridoxal phosphate; Multigene family.
FT      BINDING: 396 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ      SEQUENCE 585 AA; 65411 MW; 8AD62B62 CRC32;

Query Match      100.0%; Score 147; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 6.54e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB      166 TLKYAIKTGHPRYFNOLSTG 185
      |||||||
OY      1 TLKYAIKTGHPRYFNOLSTG 20

RESULT 4
ID      DCE2_MOUSE      STANDARD:      PRT:      585 AA.
AC      P48320; O35519;

```



DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91014554.  
 RA WYORSKI R.J., BOND R.W., GOTTLIEB D.I.;  
 RT "Characterization of a cDNA coding for rat glutamic acid  
 RT decarboxylase.";  
 RL Brain Res. Mol. Brain Res. 8:193-198(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 90132703.  
 RA JULIEN J.F., SAMAMA P., MALET J.;  
 RT "Rat brain glutamic acid decarboxylase sequence deduced from a cloned  
 RT cDNA.";  
 RL J. Neurochem. 54:703-705(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92020930.  
 RA MICHELSEN B.K., PETERSEN J.S., BOEL E., MOLDROP A., DYBERG T.,  
 RA MADSEN O.D.;  
 RT "Cloning, characterization, and autoimmune recognition of rat islet  
 RT glutamic acid decarboxylase in insulin-dependent diabetes mellitus.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
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 CC -----

Query Match 91.2% Score 134; DB 1; Length 593;  
 Best Local Similarity 80.0%; Pred. No. 1,91e-17;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRTHGHPFFNOLSTG 193  
 |||||:|||||:|||||  
 1 TLKVAIKTGHPRFFNOLSTG 20

RESULT 7

ID DCEL\_PIG STANDARD; PRT; 594 AA.  
 AC P48319;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Sus scrofa (pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 95137399.  
 RA SUZUKI R., ASAMI N., AWANN E., WAGATSUMA M.;  
 RT "Sequences of two porcine glutamic acid decarboxylases (65- and  
 RT 67-kDa GAD).";  
 RL Gene 152:257-260(1995).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC -----  
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 CC -----

Query Match 91.2% Score 134; DB 1; Length 594;  
 Best Local Similarity 80.0%; Pred. No. 1,91e-17;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Db 175 TLKYGVRTHGHPFFNOLSTG 194  
 |||||:|||||:|||||  
 1 TLKVAIKTGHPRFFNOLSTG 20

RESULT 8  
 ID DCEL\_HUMAN STANDARD; PRT; 594 AA.  
 AC O98259;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 92196068.  
 RA BU D.-F., ERLANDER M.G., HITZ B.C., TILLARATINE N.J., KAUFMAN D.L.,  
 RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;  
 RT "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are  
 RT each encoded by a single gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94375018.  
 RA BU D.-F., TOBIN A.J.;  
 RT "The exon-intron organization of the genes (GAD1 and GAD2) encoding  
 RT two human glutamate decarboxylases (GAD67 and GAD65) suggests that  
 RT they derive from a common ancestral GAD.";  
 RL Genomics 21:222-228(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 93080286.  
 RA KELLY C.D., EDWARDS Y., JOHNSTONE A.P., HARFST E., NOGRADI A.,  
 RA NUSSEY S.S., POVEY S., CARTER N.D.;  
 RT "Nucleotide sequence and chromosomal assignment of a cDNA encoding  
 RT the large isoform of human glutamate decarboxylase.";  
 RL Ann. Hum. Genet. 56:255-265(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93282844.  
 RA YAMASHITA K., GRAM D.S., HARRISON L.C.;  
 RT "Molecular cloning of full-length glutamic acid decarboxylase 67 from  
 RT human pancreas and islets.";  
 RL Biochem. Biophys. Res. Commun. 192:1347-1352(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PANCREATIC ISLETS;  
 RX MEDLINE: 93282845.  
 RA KAWASAKI E., MORIUCHI R., WATANABE M., SATOH K., BRUNICARDI F.C.,  
 RA WATT P.C., YAMAGUCHI T., MULLEN Y., AKAZAWA S., MIYAMOTO T.;  
 RT "Cloning and expression of large isoform of glutamic acid  
 RT decarboxylase from human pancreatic islet.";  
 RL Biochem. Biophys. Res. Commun. 192:1353-1359(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA GIORA R., PEAKMAN M., VERGANI D., TRUCCO M.;  
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE OF 218-397 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 91248209.  
 RA GRAM D.S., BARNETT L.D., JOSEPH J.L., HARRISON L.C.;  
 RT "Cloning and partial nucleotide sequence of human glutamic acid  
 RT decarboxylase cDNA from brain and pancreatic islets.";  
 RL Biochem. Biophys. Res. Commun. 176:1239-1244(1991).  
 RN [8]  
 RP SEQUENCE OF 527-594 FROM N.A.  
 RC TISSUE-TESTIS;  
 RX MEDLINE: 90355986.  
 RA PERSSON H., PELTO-HUUKKO M., METSIS M., SOEDER O., BRENE S.,  
 RA SKOG S., HOKKFELT T., RITZEN E.M.;  
 RT "Expression of the neurotransmitter-synthesizing enzyme glutamic acid  
 RT decarboxylase in male germ cells.";  
 RL Mol. Cell. Biol. 10:4701-4711(1990).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
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 CC -----  
 CC EMBL: M81883; AAA62368.1; -  
 CC EMBL: L16888; AAB59427.1; -  
 CC EMBL: 222750; CAA80435.1; -  
 CC EMBL: S61897; AAB26937.1; -  
 CC EMBL: S61898; AAB26938.1; -

DR EMBL: M86522; AAA35900.1; -  
 DR EMBL: M70434; AAA52512.1; -  
 DR EMBL: M55574; AAA72938.1; -  
 DR EMBL: A28074; CAA01913.1; -  
 DR PIR: P00157; P00157.  
 DR MIM: 266100; -  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PRAM: PF00282; pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 405 405  
 FT CONFLICT 9 9  
 FT CONFLICT 16 17  
 FT CONFLICT 17 17  
 FT CONFLICT 18 18  
 FT CONFLICT 31 31  
 FT CONFLICT 68 68  
 FT CONFLICT 116 116  
 FT CONFLICT 136 136  
 FT CONFLICT 140 140  
 FT CONFLICT 142 142  
 FT CONFLICT 155 155  
 FT CONFLICT 206 206  
 FT CONFLICT 302 302  
 FT CONFLICT 436 436  
 FT CONFLICT 512 512  
 FT CONFLICT 477 477  
 FT CONFLICT 492 492  
 FT CONFLICT 565 565  
 SQ SEQUENCE 594 AA; 66896 MM; 94733552 CAC32;  
 Query Match 91.2%; Score 134; DB 1; Length 594;  
 Best Local Similarity 80.0%; Pred. No. 1.91e-17;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 Db 175 TLKXGVRTHGPRFNOUSTG 194  
 QY 1 TLKXIRKTHGPRFNOUSTG 20  
 |||||:|||||:|||||  
 ID DCGL FELCA STANDARD; PRT; 594 AA.  
 AC P14748;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-OCIPITAL CORTEX;  
 RX MEDLINE: 87310623.  
 RA KOBAYASHI Y., KAUFMAN D.L., TOBIN A.J.;  
 RT "Glutamic acid decarboxylase cDNA: nucleotide sequence encoding an  
 RT enzymatically active fusion protein.";  
 RL J. Neurosci. 7:2768-2772(1987).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC -----  
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CC -----
CC EMBL; M18629; AAA51430.1; -.
CC DR PIR; A45671; A45671.
CC DR PIR; A46758; A46758.
CC DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
CC DR PFAM; PF00282; pyridoxal_dec; 1.
CC DR Neurotransmitter_biosynthesis; Lyase; Decarboxylase;
CC KM Pyridoxal phosphate; Multigene family.
CC FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
CC SO SEQUENCE 594 AA; 66824 MW; 3EC20778 CRC32;
CC
CC Query Match 91.2%; Score 134; DB 1; Length 594;
CC Best Local Similarity 80.0%; Pred. No. 1,91e-17;
CC Matches 16; Conservative 4; Mismatches 0; Gaps 0;
CC
CC Db 175 TLKGYVTRTGHPRFENQSTNG 194
CC Oy 1 TLKTAIKTGHPRFENQSTNG 20
CC
CC RESULT 10
CC ID DCE DROME STANDARD; PRF: 510 AA.
CC AC P20228;
CC DT 01-FEB-1991 (Rel. 17, Created)
CC DT 01-FEB-1991 (Rel. 17, Last sequence update)
CC DT 01-NOV-1995 (Rel. 32, Last annotation update)
CC DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).
CC GN GAD OR GIB.
CC OS Drosophila melanogaster (Fruit fly).
CC OC Euarystota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC OC Eurytota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC NC Ephydroidea; Drosophilidae; Drosophila.
CC RC [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE; 90155291.
CC RA JACKSON F.R., NEMBY L.M., KULKARNI S.J.;
CC R# "Drosophila GABAergic systems: sequence and expression of glutamic
CC RL acid decarboxylase.";
CC J. Neurochem. 54:1068-1078(1990).
CC CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC CC -1- SUBUNIT: HOMODIMER.
CC CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC CC -----
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CC CC -----
CC CC EMBL; X76198; CAA53791.1; -.
CC DR PIR; A30999; A30999.
CC DR PIR; JH0192; JH0192.
CC DR FLXBASE; P800004516; Gad1.
CC DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
CC DR PFAM; PF00282; Pyridoxal_dec; 1.
CC KM Neurotransmitter_biosynthesis; Lyase; Decarboxylase;
CC KW Pyridoxal phosphate.
CC FT BINDING 322 322 PYRIDOXAL PHOSPHATE (POTENTIAL).
CC SO SEQUENCE 510 AA; 57758 MW; 97C7A8F1 CRC32;
CC
CC Query Match 83.7%; Score 123; DB 1; Length 510;
CC Best Local Similarity 75.0%; Pred. No. 1,40e-14;
CC Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC
CC Db 92 TLKGYVTRTGHPRFENQSTNG 111
CC Oy 1 TLKTAIKTGHPRFENQSTNG 20

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RESULT 11 STANDARD: PRT: 413 AA.
ID YG10_ECOLI
AC Q46861;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHEETICAL 46.9 KD PROTEIN IN METC-SUFI INTERGENIC REGION.
GN YG10.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
OC [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655.
RX MEDLINE: 97426617.
RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V., RILEY M., COLLADO-VIDES J., GLASNER E.D., RODE C.K., MAYHEW G.F., RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J., MAU B., SHAO Y.
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC -1- SIMILARITY: TO THE C-TERMINAL OF M.JANNASCHII M1155. THE N-TERMINAL PART OF M1155 IS COLINEAR TO E.COLI YG1R. ALSO SOME SIMILARITY TO FAMILY UPF0004.
CC CC
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or\_send\_an\_email\_to\_license@sib-sib.ch).
CC CC
CC CC EMBL: U28377; AAA69183.1; -
DR EMBL: AE000383; AAC76051.1; -
DR ECGENE: EG15019; YG10.
KW Hypothetical protein.
SQ SEQUENCE 413 AA; 46943 MW; 8E9159B5 CRC32;

Query Match 46.9% Score 69 DB 1; Length 413;
Best Local Similarity 38.9% Pred No. 6.51e-02;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Db 170 VRYDIAPEDPRYKIELAT 187
oy 2 LKYAIKGTGHPRYENQNST 19
:::| |:::| |
:::| |:::| |

RESULT 12 STANDARD: PRT: 391 AA.
ID PYRC_USTMA
AC P31301;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE DIHYDROROTASE (EC 3.5.2.3) (DHORASE).
GN PYR3.
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OC [1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-521;
RX MEDLINE: 92354940.
RA SPANOS A., KANDUGA N., HOLDEN D.W., BANKS G.R.;
RT "The Ustilago maydis pyr3 gene: sequence and transcriptional analysis."
RT Gene 117:73-79(1992).
CC -1- CATALYTIC ACTIVITY: DIHYDROROTATE + H(2)O -> N-CARBAMOYL-L-ASPARATE.
CC -1- COFACTOR: ZINC.
CC -1- PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.

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Query Match 44.2% Score 65; DB 1; Length 897;  
 Best Local Similarity 50.0%; Pred. No. 4.02e-01;  
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 DB 484 KYLAKSGLOKYNOLG 499  
 QY 3 KYAKTGHPRYFNLS 18

RESULT 15  
 ID YEBA\_HAEIN STANDARD; PRT; 475 AA.  
 AC P44693;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE HYPOTHETICAL PROTEIN HI0409.  
 GN HI0409.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Haemophilus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RD / KW20;  
 RX MEDLINE: 95350630.  
 RA FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,  
 KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,  
 MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,  
 SCOTT J.D., SHIRLEY R., LIU L.-I., GLODER A., KELLEY J.M.,  
 WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLUM E., COTTON M.D.,  
 UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C.,  
 RA FINE L.D., FRITCHMAN J.L., FUHRMAN J.L., GEOGHAGEN N.S.M.,  
 GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,  
 RA VENTER J.C.,  
 RT "Whole-genome random sequencing and assembly of Haemophilus  
 influenzae Rd.";  
 RL Science 269:496-512(1995).  
 CC -!- FUNCTION: COULD BE INVOLVED IN CELL WALL DEGRADATION OR  
 FORMATION (BY SIMILARITY).  
 CC -!- SIMILARITY: STRONG, TO E.COLI YEBA.  
 CC -!- SIMILARITY: TO STAPHYLOCOCCUS LYSOSTAPHIN.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: U3724; AAC22068.1; -.  
 DR TIGR: H10409; -.  
 DR PFAM: PF01551; Peptidase\_M37; 1.  
 DR Hypothetical protein; Cell wall.  
 KW SEQUENCE 475 AA; 53255 MW; 8C160515 CRC32;

Query Match 43.5% Score 64; DB 1; Length 475;  
 Best Local Similarity 46.2%; Pred. No. 6.27e-01;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

DB 297 YAVQANGRYNO 309  
 QY 4 YAIKTGHPRYFNQ 16

Search completed: Tue Mar 7 21:30:35 2000  
 Job time : 6 secs.





RA WABERG F.:  
 RT "Characterization of glutamate decarboxylase in chicken."  
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.  
 CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYDCC).  
 CC EMBL: AF030355; AAD01902.1; -.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 KM Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 590 AA; 66710 MW; 808650FF CRC32;

Query Match 91.2%; Score 134; DB 13; Length 590;  
 Best Local Similarity 80.0%; Pred. No. 6,34e-18;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 171 TLKYGVRGTGHPREFNOLSTG 190  
 |||:::||||:|||||  
 QY 1 TLKYAIKTGHPREFNOLSTG 20

RESULT 3  
 ID 008685 PRELIMINARY; PRT; 593 AA.  
 AC 008685;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE 67KD GLUTAMIC ACID DECARBOXYLASE.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C.  
 RA AUST G., STEINBRENNER H., THAMM B., ROST A.K., SEISSLER J.;  
 RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.  
 CC -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYDCC).  
 CC EMBL: Y12257; CAN72934.1; -.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFM: PF00282; Pyridoxal\_dec; 1.  
 KM Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 593 AA; 66648 MW; BAFE92E0 CRC32;

Query Match 91.2%; Score 134; DB 11; Length 593;  
 Best Local Similarity 80.0%; Pred. No. 6,34e-18;  
 Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Db 174 TLKYGVRGTGHPREFNOLSTG 193  
 |||:::||||:|||||  
 QY 1 TLKYAIKTGHPREFNOLSTG 20

RESULT 4  
 ID 044102 PRELIMINARY; PRT; 370 AA.  
 AC 044102;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).  
 GN GAD1.  
 OS Drosophila pseudoobscura (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC ZENG L.-W., COMERON J.M., CHEN B., KREITMAN M.;  
 RL Genetica 0:0-0(1997).  
 DR EMBL: AF025807; AAB87892.1; -.  
 DR HSSP: P06543; 100C.  
 DR FLYBASE: FBgn0023295; Dpse\Gad1.  
 DR PFM: PF00282; Pyridoxal\_dec; 2.

FT NON\_TER 1 1  
 FT NON\_TER 370 370  
 SQ SEQUENCE 370 AA; 41887 MW; A1EB456F CRC32;

Query Match 83.7%; Score 123; DB 5; Length 370;  
 Best Local Similarity 75.0%; Pred. No. 5,61e-15;  
 Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 12 TLKYVKTGHPREFNOLSTG 31  
 |||:||||:|||||  
 QY 1 TLKYAIKTGHPREFNOLSTG 20

RESULT 5  
 ID 044103 PRELIMINARY; PRT; 370 AA.  
 AC 044103;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).  
 GN GAD1.  
 OS Drosophila subobscura (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC ZENG L.-W., COMERON J.M., CHEN B., KREITMAN M.;  
 RL Genetica 0:0-0(1997).  
 DR EMBL: AF025808; AAB87893.1; -.  
 DR HSSP: P06543; 100C.  
 DR FLYBASE: FBgn0023244; Dsub\Gad1.  
 DR PFM: PF00282; Pyridoxal\_dec; 2.  
 FT NON\_TER 1 1  
 FT NON\_TER 370 370  
 SQ SEQUENCE 370 AA; 41923 MW; D75BDC49 CRC32;

Query Match 83.7%; Score 123; DB 5; Length 370;  
 Best Local Similarity 75.0%; Pred. No. 5,61e-15;  
 Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 12 TLKYVKTGHPREFNOLSTG 31  
 |||:||||:|||||  
 QY 1 TLKYAIKTGHPREFNOLSTG 20

RESULT 6  
 ID 09Y602 PRELIMINARY; PRT; 267 AA.  
 AC 09Y602;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 1.  
 GN CSAD.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RC PRITCHARD J.E., RAMSDEN D.B.;  
 RT "Human cysteine sulfinic acid decarboxylase (CSAD)-related mRNA, 1.";  
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF116545; AAD2543.1; -.  
 SQ SEQUENCE 267 AA; 30264 MW; A3475A7D CRC32;

Query Match 76.9%; Score 113; DB 4; Length 267;  
 Best Local Similarity 63.2%; Pred. No. 2,33e-12;  
 Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Db 78 IRYSVKTGHPREFNOLSTG 96  
 ::|||:||||:||||:|  
 QY 2 LKYAIKTGHPREFNOLSTG 20

RESULT	7			
ID	Q9Y600.	PRELIMINARY:	PRT:	493 AA.
AC	Q9Y600.			
DT	01-NOV-1999 (TREMBLrel, 12, Created)			
DD	01-NOV-1999 (TREMBLrel, 12, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel, 12, Last annotation update)			
DE	CYS-LEU SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 3. CSAD.			
GN	Homo sapiens (Human).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Mammalia;			
NC	Eukarya; Primates; Catarrhini; Homidae; Homo.			
NN	[1]			
NP	SEQUENCE FROM N.A.			
RC	TISSUE-BRAIN:			
RA	PRITCHARD J.E., RAMSDEN D.B.;			
RT	"Human cysteine sulfinic acid decarboxylase (CSAD)-related mRNA, 3.";			
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF116547; AAD32545.1; "			
SQ	SEQUENCE 493 AA: 54951 MW: F4852742 CRC32:			
Query Match	76.9%;	Score 113;	DB 4;	Length 493;
Best Local Similarity	63.2%;	Pred. No. 2.33e-12;		
Matches 12;	Conservative	6;	Mismatches 1;	Indels 0;
Gaps				0.
Db	78 IRISVKTGHPRFNFOLFSG 96			
	:::::::::::::::::::::			
oy	2 LKTAIKTGHPRFNFOLFSTG 20			

RESULT	8	PRELIMINARY;	PRT;	78 AA.
ID	P70713			
AC	P70713.			
DT	01-FEB-1997 (TREMBLrel. 02, Created)			
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)			
DT	01-MAY-1999 (TREMBLrel. 10, Last annotation update)			
DE	(CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29))			
DE	(SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE)			
DE	(FRAGMENT).			
OS	Rattus norvegicus (Rat).			
OC	Euarctia; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-SPRAGUE-DAWLEY; TISSUE=LIVER;			
RA	KRATSKIN I. L., YU X., SMUTZER G., DOTY R. L.;			
RL	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE = HYPOTAURINE + CO(2).			
CC	-1- COPACTOR: PYRIDOXAL-PHOSPHATE.			
DR	EMBL; U74492; AAB18332.1; -			
DR	PFAM; PF00282; Pyridoxal_dec; 1.			
KW	Lysase.			
FT	NON_TER	1	1	
FT	NON_TER	78	78	
SO	SEQUENCE	78 AA;	9134 MW;	F4808DJF CRC32;
	Query Match	73.5%;	Score 108;	DB 11; Length 78;
	Best Local Similarity	63.2%;	Pred. No. 4,48e-11;	
	Matches 12; Conservative	5;	Mismatches 2;	Indels 0; Gaps 0
DB	37 IH5YKGTGHPRFNFOLFSG 55			
	.:.:.:.:.:.:.:.:.:.:.:.			
OY	2 LKFAIKGTGHPRFNFOLFSG 20			
RESULT	9	PRELIMINARY;	PRT;	478 AA.
ID	O64577			
AC	O64577.			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)			

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OS (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).
OC Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY;
RX MEDLINE; 95290489.
RA KATSAVIA P.J., JERKINS A.A., GOODSPEED D.C., STEELE R.D.;
RT "Cloning and characterization of rat cysteine sulfinate acid
RT decarboxylase."
RL Biochim. Biophys. Acta 1262:79-82(1995).
CC -1- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE = HYDROTURINE + CO(2).
CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE. (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
DR EMBL; M64755; AAC42063.1; -.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFM; PF00282; pyridoxal_dec; 1.
SQ Lysase: Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 478 AA; 53725 MW; 4CAC0093 CRC32.

Query Match 73.5%; Score 108; DB 11; Length 478;
Best Local Similarity 63.2%; Pred. No. 4,48e-11;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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[illegible]

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DI 01-NOV-1999 (TEMBLrel. 12, last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE.
GNC -25 OR Y37D8A.23.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL.
RX MEDLINE: 99098940.
RA JIN Y., JORGENSEN E., HARTWIG E., HORVITZ H.R.:
RT "The Caenorhabditis elegans gene unc-25 encodes glutamic acid
RT decarboxylase and is required for synaptic transmission but not
RT synaptic development."
RT J. Neurosci. 19:539-548(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-C.elegans;
RX BAKLOW K.:
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-C.elegans;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LARRELLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALLDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.:
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RT Nature 368:32-38(1994).
RL EMBL: AF109378; AAD19958.1; -.
DR EMBL: AL032626; CAA21537.1; -.
SQ SEQUENCE 508 AA; 57792 MW; 3A3E7F33 CRC32;

Query Match 65.3%; Score 96; DB 5; Length 508;
Best Local Similarity 57.9%; Pred. No. 4,48e-06;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Db 91 LRLGRTGHPREFNOISG 109
QY 2 LKVAIKTGHPRFNOISTG 20

RESULT 12
ID 024062 PRELIMINARY; PRT; 575 AA.
AC 024062;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, last annotation update)
DE GLUTAMATE DECARBOXYLASE.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Ephygotea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R; TISSUE-NEURAL;
RA PHILLIPS M., SALIKOFF L., KELLY L.:
RL J. Neurochem. 0:0-0(0).
DR EMBL: U01239; AAC46466.1; -.
DR FLYBASE: FBgn0005622; Gad2.
DR PFAM: PF00282; Pyridoxal dec. 1.
SQ SEQUENCE 575 AA; 64795 MW; 3CFA48E5 CRC32;

Query Match 59.2%; Score 87; DB 5; Length 575;

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Best Local Similarity 50.0%; Pred. No. 6,52e-06;
Matches 10; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Db 156 TIRSVKTHPRFINDYSG 175
QY 1 LKVAIKTGHPRFNOISTG 20

RESULT 13
ID 043308 PRELIMINARY; PRT; 1224 AA.
AC 043308;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, last sequence update)
DT 01-AUG-1998 (TEMBLrel. 07, last annotation update)
DE KIAA0425.
GNC KIAA0425.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA ISHIKAWA K., NAGASE T., NAKAJIMA D., SEKI N., OHIRA M., MIYAJIMA N.,
RA TANAKA A., KOTANI H., NOMURA N., OHARA O.:
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB007885; BAA24855.1; -.
SQ SEQUENCE 1224 AA; 136329 MW; 8E27BD0D CRC32;

Query Match 46.3%; Score 68; DB 4; Length 1224;
Best Local Similarity 47.1%; Pred. No. 1,11e-01;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Db 1089 TLKSTKMTLRFPPPL 1105
QY 1 LKVAIKTGHPRFNOI 17

RESULT 14
ID 09W668 PRELIMINARY; PRT; 77 AA.
AC 09W668;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, last annotation update)
DE MATRIX GLA PROTEIN (FRAGMENT).
GNC MGP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA CANCELA M.L.:
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF055588; AAD28354.1; -.
FT NON-TER
SQ SEQUENCE 77 AA; 9406 MW; 3DB2A863 CRC32;

Query Match 45.6%; Score 67; DB 13; Length 77;
Best Local Similarity 37.5%; Pred. No. 1,79e-01;
Matches 6; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 56 ALRYGTAAYKRYFGQ 71
QY 1 LKVAIKTGHPRFNO 16

RESULT 15
ID 029449 PRELIMINARY; PRT; 1149 AA.
AC 029449;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 09, last sequence update)
DT 01-MAY-1999 (TEMBLrel. 10, last annotation update)
DE CHROMAFIN GRANULE ATPASE II.

```

OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
OC Bovinae; Bos.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE; 96234315.  
RA TANG X., HALBECK M.S., SCHLEGEL R.A., WILLIAMSON P.;  
RT "A subfamily of P-type ATPases with aminophospholipid transporting  
RT activity.";  
RL Science 272:1495-1497(1996).  
DR EMBL: U51100; AAD03352.1; -;  
DR PFAM: PF00122; E1-E2\_ATPase; 4.  
KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.  
FT MOD\_RES 409 409 PHOSPHORYLATION (PROBABLE).  
SQ SEQUENCE 1149 AA; 130025 MW; 73850931 CRC32;

Query Match 44.2% Score 65; DB 6; Length 1149;  
Best Local Similarity 50.08; Pred. No. 4.60e-01;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

DB 733 TKYALTFGVQYFLDIA 750  
|||||:|:|:|:|:  
QY 1 TKYAIKTGHRXYFNQLS 18

Search completed: Tue Mar 7 21:34:11 2000  
Job time : 12 secs.

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\*\*\*\*\*  
(TM)

Msearch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:43:46 2000; MasPar time 5.51 Seconds  
Tabular output not generated. 171.121 Million cell updates/sec

Title: >US-08-981-824-5  
Description: (1-20) from US08981824.pep  
Perfect Score: 135  
Sequence: 1 PRYFNOLSTGLDMVGLADW 20

Scoring table: PAM 150  
Gap 15

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: plr62  
1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 30.321; Variance 45.070; scale 0.673

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	155	100.0	205	2	65 kda glutamate deca	3.18e-19
2	155	100.0	585	1	glutamate decarboxyla	3.18e-19
3	155	100.0	585	1	glutamate decarboxyla	3.18e-19
4	155	100.0	585	1	glutamate decarboxyla	3.18e-19
5	155	100.0	585	1	glutamate decarboxyla	3.18e-19
6	135	87.1	585	2	glutamate decarboxyla	1.57e-14
7	135	87.1	585	2	glutamate decarboxyla	1.57e-14
8	135	87.1	585	2	glutamate decarboxyla	1.57e-14
9	135	87.1	585	2	glutamate decarboxyla	1.57e-14
10	135	87.1	585	2	glutamate decarboxyla	1.57e-14
11	135	87.1	585	2	glutamate decarboxyla	1.57e-14
12	135	87.1	585	2	glutamate decarboxyla	1.57e-14
13	135	87.1	585	2	glutamate decarboxyla	1.57e-14
14	135	87.1	585	2	glutamate decarboxyla	1.57e-14
15	135	87.1	585	2	glutamate decarboxyla	1.57e-14
16	80	51.6	493	2	glutamate decarboxyla	5.13e-10
17	80	51.6	493	2	glutamate decarboxyla	5.13e-10
18	80	51.6	493	2	glutamate decarboxyla	5.13e-10
19	80	51.6	493	2	glutamate decarboxyla	5.13e-10
20	80	51.6	493	2	glutamate decarboxyla	5.13e-10
21	80	51.6	493	2	glutamate decarboxyla	5.13e-10
22	80	51.6	493	2	glutamate decarboxyla	5.13e-10
23	80	51.6	493	2	glutamate decarboxyla	5.13e-10

24	64	41.3	796	2	A45695	capsid precursor - hu	6.27e+00
25	63	40.6	409	2	S53303	aspartate transaminas	9.16e+00
26	62	40.0	294	2	D70525	probable beta-1 - Myc	1.33e+01
27	62	40.0	344	2	H64477	malate dehydrogenase	1.33e+01
28	62	40.0	407	2	JC5124	aspartate transaminas	1.33e+01
29	62	40.0	552	2	JQ1193	cholesterol oxidase (	1.33e+01
30	62	40.0	575	1	JH0827	glutamate decarboxyla	1.33e+01
31	61	39.4	216	2	S58552	hypothetical protein	1.93e+01
32	61	39.4	360	2	S58205	DHR38 protein - silk	1.93e+01
33	61	39.4	453	2	S39927	aspartate transaminas	1.93e+01
34	61	39.4	453	2	S39928	aspartate transaminas	1.93e+01
35	61	39.4	454	1	XNYE16	aspartate transaminas	1.93e+01
36	61	39.4	455	2	S46316	aspartate transaminas	1.93e+01
37	61	39.4	463	2	S33528	aspartate transaminas	1.93e+01
38	61	39.4	463	2	A40013	phosphomannomutase (E	1.93e+01
39	61	39.4	463	2	S39926	aspartate transaminas	1.93e+01
40	61	39.4	463	2	S39925	aspartate transaminas	1.93e+01
41	61	39.4	538	1	D64164	hypothetical protein	1.93e+01
42	61	39.4	661	2	S75005	sensory transduction	1.93e+01
43	60	38.7	1375	2	F48216	neurexin IIF-alpha se	2.78e+01
44	60	38.7	1471	2	B48218	neurexin IIF-alpha me	2.78e+01
45	60	38.7	1578	2	I48216	neurexin IIF-alpha me	2.78e+01

## ALIGNMENTS

RESULT 1  
ENTRY 1  
TITLE 167412 #type fragment  
ORGANISM 65 kda glutamate decarboxylase, brain - mouse (fragment)  
DATE 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 30-May-1997

ACCESSIONS  
REFERENCE I53274  
#authors Faulkner-Jones, B.E.; Gram, D.S.; Kun, J.; Harrison, L.C.  
#journal Endocrinology (1993) 133:2962-2972  
#title Localization and quantitation of expression of two glutamate decarboxylase genes in pancreatic beta-cells and other peripheral tissues of mouse and rat.  
#cross-references MVID:94062679  
#accession I67412  
##status preliminary; translated from GB/EMBL/DBJ  
##molecule\_type mRNA  
##residues 1-205 #label RES  
##cross-references GB:S67454; NID:9456852  
CLASSIFICATION #superfamily human glutamate decarboxylase  
SUMMARY #length 205 #checksum 3167

Query Match 100.0%; Score 155; DB 2; Length 205;  
Best Local Similarity 100.0%; Pred. No. 3.18e-19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 PRYFNOLSTGLDMVGLADW 21  
QY 1 PRYFNOLSTGLDMVGLADW 20

RESULT 2  
ENTRY 2  
TITLE JH0423 #type complete  
ALTERNATE\_NAMES glutamate decarboxylase (EC 4.1.1.15) 2 - rat  
ORGANISM glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
#formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 31-Mar-1992 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1998  
ACCESSIONS JH0423; A60888  
REFERENCE JH0423  
#authors Erlander, M.G.; Tiliakaratne, N.J.K.; Feldblum, S.; Patel, N.; Tobin, A.J.  
#journal Neuron (1991) 7:91-100  
#title Two genes encode distinct glutamate decarboxylases.  
#cross-references MVID:9129343  
#accession JH0423  
#molecule\_type mRNA

##residues 1-585 ##label ERL  
##cross-references GB:M7422; NID:g204225; PIDN:AAA63488.1; PID:g204226  
##experimental\_source brain  
#note the authors translated the codon GAT for residue 86 as His, TCA for residue 198 as Ala, and CAG for residue 428 as Trp

REFERENCE  
#authors A60888  
#journal Chang, Y.C.; Gottlieb, D.I.  
#title J. Neurosci. (1988) 8:2123-2130  
Characterization of the proteins purified with monoclonal antibodies to glutamic acid decarboxylase.  
#cross-references MUID:88258610  
#accession A60888  
#status preliminary  
#molecule\_type protein  
#residues 'V',191-194,'X',196-203,'XX',206-219,'X',225-234,'X',236-247,'X',249-266,'X',524-537,539-543,'V',547-549,'X',551-553,'X',555-558 ##label CHA  
'X',551-553,'X',555-558 ##label CHA

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase  
K1760P05 carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE  
396 #binding\_site pyridoxal phosphate (lys) (covalent)  
#status predicted

SUMMARY #length 585 #molecular-weight 65402 #checksum 7756

Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 3,18e-19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 176 PRYFMOLSTGLDMVGLADW 195  
|||||  
Oy 1 PRYFMOLSTGLDMVGLADW 20

RESULT 3  
ENTRY A41292 #type complete  
ENTRY glutamate decarboxylase (EC 4.1.1.15) 2 - human  
TITLE glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ALTERNATE\_NAMES #formal\_name Homo sapiens #common\_name man  
ORGANISM 13-May-1992 #sequence\_revision 23-Mar-1995 #text\_change  
DATE 18-Jun-1999

ACCESSIONS A41935; A41292; S30058; B54778  
REFERENCE A41935  
#authors Bu, D.F.; Erlender, M.G.; Hiltz, B.C.; Tiliakarane, N.J.K.; Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J.

#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.  
#cross-references MUID:92196068  
#accession A41935  
#molecule\_type mRNA  
#residues 1-585 ##label BU1  
##cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934  
##experimental\_source brain  
#note sequence extracted from NCHI backbone (NCBI:88007)

REFERENCE A41292  
#authors Karlsson, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.; Distcheche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.; Grant, F.J.; Foster, D.; Lernermark, A.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341  
#title Cloning and primary structure of a human islet isoform of glutamic acid decarboxylase from chromosome 10.  
#cross-references MUID:92020848  
#accession A41292  
#molecule\_type mRNA  
#residues 1-585 ##label KAR  
##cross-references GB:M74826; NID:g182931; PIDN:AAA56491.1; PID:g182932  
#experimental\_source pancreatic islet

REFERENCE S30058  
#authors Mauch, L.; Abney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel, B.; Northemann, W.  
#journal Eur. J. Biochem. (1993) 212:597-603  
#title Characterization of a linear epitope within the human pancreatic 64-kDa glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients.  
#cross-references MUID:93185681  
#accession S30058  
#molecule\_type mRNA  
#residues 6-585 ##label MAU  
##cross-references EMBL:X6936  
#experimental\_source pancreatic islet

REFERENCE A54778  
#authors Bu, D.F.; Tobin, A.J.  
#journal Genomics (1994) 21:222-228  
#title The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral GAD.

##cross-references MUID:94375018  
#contents annotation: intron-exon boundaries

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene. GAD has also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.

GENETICS  
#gene GDB:GAD2  
##cross-references GDB:128595; OMIM:138275  
#map\_position 10p11.23-10p11.23

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE  
396 #binding\_site pyridoxal phosphate (lys) (covalent)  
#status predicted

SUMMARY #length 585 #molecular-weight 65411 #checksum 4799

Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 3,18e-19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 176 PRYFMOLSTGLDMVGLADW 195  
|||||  
Oy 1 PRYFMOLSTGLDMVGLADW 20

RESULT 4  
ENTRY S38533 #type complete  
ENTRY glutamate decarboxylase (EC 4.1.1.15) 2 - mouse  
TITLE glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ALTERNATE\_NAMES #formal\_name Mus musculus #common\_name house mouse  
ORGANISM 20-May-1994 #sequence\_revision 23-Mar-1995 #text\_change  
DATE 18-Jun-1999

ACCESSIONS S38533  
REFERENCE S38533  
#authors Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.  
#journal Biochim. Biophys. Acta (1993) 1216:157-160  
#title Cloning and sequence analysis of a murine cDNA encoding glutamate decarboxylase (GAD65).  
#cross-references MUID:94032481  
#accession S38533  
#status preliminary  
#molecule\_type mRNA  
#residues 1-585 ##label IEE  
##cross-references GB:IL1980; NID:g413867; PIDN:AAA93049.1; PID:g413868  
#experimental\_source brain

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal



FEATURE phosphate  
396 #binding\_site pyridoxal phosphate (Lys) (covalent)  
#status Predicted  
SUMMARY #length 585 #molecular-weight 65224 #checksum 7599  
Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 3.18e-19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 176 PRFNOLSTGLDMVGLAADM 195  
QY 1 PRFNOLSTGLDMVGLAADM 20

RESULT 5  
ENTRY JC4064 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 65K chain - pig  
ORGNANISM #formal\_name Sus scrofa domestica #common\_name domestic pig  
DATE 30-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 22-Jun-1999  
ACCESSIONS JC4064  
REFERENCE JC4064  
#authors Suzuki, R.; Asami, N.; Amann, E.; Magatsuma, M.  
#journal Gene (1995) 152:257-260  
#title Sequences of two porcine glutamic acid decarboxylases (65-and 67-kDa GAD).  
#cross-references MUID:95137399  
#accession JC4064  
#molecule\_type mRNA  
#residues 1-585 #label SUZ  
#cross-references DDBJ:D31848; NID:9790964; PIDN:BA06635.1; PID:d1007207; PID:9790965  
#experimental\_source brain  
COMMENT This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
FEATURE 393-396 #domain DOPA decarboxylase binding #status predicted  
SUMMARY #length 585 #molecular-weight 65388 #checksum 5933  
Query Match 100.0%; Score 155; DB 2; Length 585;  
Best Local Similarity 100.0%; Pred. No. 3.18e-19;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 176 PRFNOLSTGLDMVGLAADM 195  
QY 1 PRFNOLSTGLDMVGLAADM 20

RESULT 6  
ENTRY I59173 #type complete  
TITLE glutamate decarboxylase - rat  
ORGNANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 22-Jun-1999  
ACCESSIONS I59173  
REFERENCE I59173  
#authors Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8771-8775  
#title Developmentally regulated expression of an exon containing a stop codon in the gene for glutamic acid decarboxylase.  
#cross-references MUID:91062362  
#accession I59173  
#status preliminary; translated from GB/EMBL/DBJ  
#molecule\_type mRNA  
#residues 1-223 #label RES  
#cross-references GB:M38350; NID:9204231; PIDN:AAA41185.1; PID:g204232  
CLASSIFICATION #superfamily human glutamate decarboxylase  
SUMMARY #length 223 #molecular-weight 25069 #checksum 1388

Query Match 87.1%; Score 135; DB 2; Length 223;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
Db 184 PRFNOLSTGLDITGLAGEW 203  
QY 1 PRFNOLSTGLDITGLAGEW 20

RESULT 7  
ENTRY S61534 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 62K isoform - mouse  
ALTERNATE\_NAMES glutamic acid decarboxylase  
ORGNANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 22-Jun-1999  
ACCESSIONS S61534  
REFERENCE S61534  
#authors Katarova, Z.; Szabo, G.; Mugnaini, E.; Greenspan, R.J.  
#journal Eur. J. Neurosci. (1990) 2:190-202  
#title Molecular identification of the 62 kd form of glutamic acid decarboxylase from the mouse.  
#accession S61534  
#molecule\_type mRNA  
#residues 1-585 #label KAT  
#cross-references EMBL:Z4976  
#experimental\_source brain  
REFERENCE S61533  
#authors Szabo, G.  
#submission submitted to the EMBL Data Library, June 1995  
#accession S61533  
#molecule\_type mRNA  
#residues 1-554, 'YQPGDKANFRMYISNPASQSDIDFLTEIERLGODL' #label 52A  
#cross-references EMBL:Z4976; NID:9886686; PIDN:CA90277.1; PID:g886687  
#experimental\_source brain  
#note the differences at the carboxyl end are due to a frameshift error  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 585 #molecular-weight 65381 #checksum 5716  
Query Match 87.1%; Score 135; DB 2; Length 585;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
Db 184 PRFNOLSTGLDITGLAGEW 203  
QY 1 PRFNOLSTGLDITGLAGEW 20

RESULT 8  
ENTRY A41367 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - rat  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGNANISM #formal\_name Rattus norvegicus #common\_name Norway rat  
DATE 12-Jun-1992 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999  
ACCESSIONS A41367; A43756; JH0195  
REFERENCE A41367  
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.; Dyberberg, T.; Madsen, O.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
#title Cloning, characterization, and autoimmune recognition of rat islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.  
#cross-references MUID:92020930  
#accession A41367  
#status preliminary  
#molecule\_type mRNA  
#residues 1-593 #label MIC  
#cross-references GB:M76177; NID:9204227; PIDN:AAA41184.1; PID:g204228

REFERENCE A43756  
#authors Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.  
#journal Brain Res. Mol. Brain Res. (1990) 8:193-198  
#title Characterization of a cDNA coding for rat glutamic acid  
decarboxylase.  
#cross-references MUID:91014554  
#accession A43756  
#status Preliminary  
##molecule-type mRNA  
##residues 1-593 ##label WYB  
##cross-references GB:X57573; NID:956183; PIDN:CAA40801.1; PID:956184  
##note The authors translated the codon TGT for residue 412 as  
Ser and TCT for residue 413 as Cys

REFERENCE JH0195  
#authors Julien, J.F.; Samama, P.; Mallet, J.  
#journal J. Neurochem. (1990) 54:703-705  
#title Rat brain glutamic acid decarboxylase sequence deduced from a  
cloned cDNA.  
#cross-references MUID:90132703  
#accession JH0195  
##molecule-type mRNA  
##residues 1-102, 'V', '104-283', 'S', '285-286', 'AD', '289-343', 'EA', '346', 'I',  
348-351, 'LE', '354-379', 'R', '381-593' ##label JUL  
#cross-references GB:X57572; NID:956185; PIDN:CAA40800.1; PID:956186  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory  
neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;  
it has several isoforms, each encoded by a separate gene.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal  
phosphate

FEATURE 404  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted

SUMMARY #length 593 #molecular-weight 66640 #checksum 3971

Query Match 87.1%; Score 135; DB 1; Length 593;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFNOLSTGLDVLGADW 203  
||:|||||||:||||:|

Qy 1 PRFNOLSTGLDVLGADW 20

RESULT 9  
ENTRY S48135 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 14-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change  
07-May-1999

ACCESSIONS S48135  
REFERENCE S48135  
#authors Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfitt, E.;  
Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.  
#journal Ann. Hum. Genet. (1992) 56:255-265  
#title Nucleotide sequence and chromosomal assignment of a cDNA  
encoding the large isoform of human glutamate  
decarboxylase.  
#cross-references MUID:93080286  
#accession S48135  
##molecule-type mRNA  
##residues 1-593 ##label KEL  
#cross-references EMBL:222750  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66952 #checksum 4836

Query Match 87.1%; Score 135; DB 2; Length 593;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFNOLSTGLDVLGADW 203  
||:|||||||:||||:|

Qy 1 PRFNOLSTGLDVLGADW 20

RESULT 10  
ENTRY S51776 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change  
16-Feb-1997

ACCESSIONS S51776  
REFERENCE S51775  
#authors Johnstone, A.  
#submission submitted to the EMBL Data Library, May 1993  
#accession S51776  
##status Preliminary  
##molecule-type mRNA  
##residues 1-593 ##label JOH  
#cross-references EMBL:222750  
##note this is an unpublished revision to the sequence from  
reference S48135

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66946 #checksum 4842

Query Match 87.1%; Score 135; DB 2; Length 593;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFNOLSTGLDVLGADW 203  
||:|||||||:||||:|

Qy 1 PRFNOLSTGLDVLGADW 20

RESULT 11  
ENTRY B41935 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change  
18-Jun-1999

ACCESSIONS B41935; JH0805; A61406; PQ0157; PQ0158; B41367;  
B41935; JH0805; A54778  
REFERENCE A41935  
#authors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tillakaratne, N.J.K.;  
Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin,  
A.J.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa  
GAD, are each encoded by a single gene.  
#cross-references MUID:92196068  
#accession B41935  
##molecule-type mRNA  
##residues 1-594 ##label BUI  
#cross-references GB:M81883; NID:9182935; PIDN:AAA62368.1; PID:9182936  
##experimental\_source pancreatic islet  
##note sequence extracted from NCBI backbone (NCBIP:88006)

REFERENCE JH0805  
#authors Kawasaki, E.; Moriuchi, R.; Watanabe, M.; Saitoh, K.; Charles  
Brunicardi, F.; Watt, P.C.; Yamaguchi, T.; Mullen, Y.;  
Akazawa, S.; Miyamoto, T.; Nagataki, S.  
#journal Biochem. Biophys. Res. Commun. (1993) 192:1353-1359  
#title Cloning and expression of large isoform of glutamic acid  
decarboxylase from human pancreatic islet.  
#cross-references MUID:93282845  
#accession JH0805  
##molecule-type mRNA  
##residues 1-17, 'N', '19-30', 'N', '32-67', 'K', '69-115', 'L', '117-154', 'T',  
156-301, 'C', '303-476', 'G', '478-491', 'G', '493-594' ##label  
KAW  
#cross-references GB:S61898; NID:9385310; PIDN:AA26998.1; PID:9385311  
##experimental\_source pancreatic islet  
REFERENCE JH0806  
#authors Yamashita, K.; Cram, D.S.; Harrison, L.C.

#journal Biochem. Biophys. Res. Commun. (1993) 192:1347-1352  
#title Molecular cloning of full-length glutamic acid decarboxylase  
#accession JH0806  
#cross-references MUID:93282844  
#molecule\_type mRNA  
#residues 1-67, 'K', 69-435, 'L', 437-511, 'S', 513-594 ##label YAM  
#cross-references GB:S61897; NID:g935450; PIDN:AA820937.1; PID:g385451  
#experimental\_source pancreatic islet  
REFERENCE  
#authors Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.  
#journal Lancet (1991) 338:1468-1469  
#title Cloning of large isoform of human brain glutamic acid  
#cross-references MUID:92065769  
#accession A61406  
#molecule\_type mRNA  
#residues 62-67, 'K', 69-205, 'N', 207-564, 'L', 566-594 ##label KEL  
#experimental\_source brain  
REFERENCE  
#authors Gram, D.S.; Barnett, L.D.; Joseph, J.T.; Harrison, L.C.  
#journal Biochem. Biophys. Res. Commun. (1991) 176:1239-1244  
#title Cloning and partial nucleotide sequence of human glutamic  
#cross-references MUID:91248209  
#accession P00157  
#molecule\_type mRNA  
#residues 218-463 ##label CR1  
#cross-references GB:M70434  
#experimental\_source brain  
#accession P00158  
#molecule\_type mRNA  
#residues 218-234, 'K', 236-240, 'N', 242-288, 'H', 290-323, 'L', 325-329,  
#cross-references GB:M70435; NID:g182941; PIDN:AA55213.1; PID:g182942  
#experimental\_source pancreatic islet  
REFERENCE  
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;  
Dyrberg, T.; Madsen, O.D.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
#title Cloning, characterization, and autoimmuno recognition of rat  
#cross-references MUID:92020930  
#accession B41367  
#molecule\_type mRNA  
#residues 317-482, 'R', 484-554 ##label MIC  
REFERENCE  
#authors Persson, H.; Peltto-Huikko, M.; Metsis, M.; Soeder, O.; Brene, S.; Skog, S.; Hoekfelt, T.; Ritzén, E.M.  
#journal Mol. Cell. Biol. (1990) 10:4701-4711  
#title Expression of the neurotransmitter-synthesizing enzyme  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
REFERENCE  
#authors Bu, D.F.; Tobin, A.J.  
#journal Genomics (1994) 21:222-228  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
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#molecule\_type mRNA  
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#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
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#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
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#molecule\_type mRNA  
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#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
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#accession A36463  
#molecule\_type mRNA  
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#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
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#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
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#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
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#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
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#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g182930  
#title The exon-intron organization of the genes (GAD1 and GAD2)  
#cross-references MUID:9035596  
#accession A36463  
#molecule\_type mRNA  
#residues 527-594 ##label PER  
#cross-references GB:M5574; NID:g182929; PIDN:AA72938.1; PID:g

```

#gene          GDB:GAD1: GAD
#cross-references GDB:119244; OMIM:266100
#map-position 2g31-2g31
#classification #superfamily human glutamate decarboxylase
#keywords        alternative splicing; carbon-carbon lyase; carboxy-lyase;
                  phosphoprotein; pyridoxal phosphate
FEATURE
405             #binding_site pyridoxal phosphate (lys) (covalent)
                  #status predicted
SUMMARY          #length 594 #molecular-weight 66924 #checksum 6189

Query Match      87.1%; Score 135; DB 1; Length 594;
Best Local Similarity 75.0%; Pied. No.1.57e-14;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGDIAGLAGEW 204
||:|||||:|||||:|
OY 1 PRFNOLSTGDIAGLAGEW 204

RESULT 12
ENTRY          S51775 #type complete
TITLE          glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
                22-Jun-1999
ACCESSIONS     S51775
REFERENCE      S51775
#authors       Johnstone, A.
#submission    Submitted to the EMBL Data Library, May 1993
#accession     S51775
#status        preliminary
#molecule_type mRNA
##residues     1-594 ##label JOH
#cross-references EMBL:Z22750; NID:g298098; PIDN:CAA80435.1;
                  PID:g298099
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS       carbon-carbon lyase; carboxy-lyase
SUMMARY        #length 594 #molecular-weight 66973 #checksum 6437

Query Match      87.1%; Score 135; DB 2; Length 594;
Best Local Similarity 75.0%; Pied. No.1.57e-14;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGDIAGLAGEW 204
||:|||||:|||||:|
OY 1 PRFNOLSTGDIAGLAGEW 204

RESULT 13
ENTRY          A46758 #type complete
TITLE          glutamate decarboxylase (EC 4.1.1.15) 1 - cat
ALTERNATE_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
ORGANISM        #formal_name Felis silvestris catus #common_name domestic cat
DATE            31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
                18-Jun-1999
ACCESSIONS     A46758; A45671#
REFERENCE      A46758
#authors       Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#submission    Submitted to GenBank, September 1989
#accession     A46758
#molecule_type mRNA
##residues     1-594 ##label KOB
#cross-references GB:M18659; NID:g163858; PIDN:AAA51430.1; PID:g163859
REFERENCE      A45671
#authors       Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#journal       J. Neurosci. (1987) 7:2768-2772
#title         Glutamic acid decarboxylase cDNA: nucleotide sequence
                encoding an enzymatically active fusion protein.
#cross-references MIMD:87310623
#accession     A45671
#molecule_type mRNA
#residues      1-558; 'RGTRPTFGSGSSRROLHSPITSSRR' ##label KO2
#irresidues

```

##note this sequence has been revised in reference A46758  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS #gene GAD1  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate  
FEATURE 405 #binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 594 #molecular-weight 66824 #checksum 5630

Query Match 87.1%; Score 135; DB 1; Length 594;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGLDMVGLADM 204  
1 PRFNOLSTGLDMVGLADM 20

RESULT 14  
ENTRY JC4065 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 67k chain - pig  
ORGANISM #formal\_name Sus scrofa domestica #common\_name domestic pig  
DATE 30-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 22-Jun-1999

ACCESSIONS JC4065  
REFERENCE JC4064  
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.  
#journal Gene (1995) 152:257-260  
#title Sequences of two porcine glutamic acid decarboxylases (65- and 67-kDa GAD).  
#cross-references MUID:95137399  
#accession JC4065  
##molecule\_type mRNA  
##residues 1-594 #label SUZ  
##cross-references DDBJ:D31849; NID:g790966; PIDN:BA06636.1; PID:d1007208; PID:g790967

COMMENT #experimental source brain  
This enzyme catalyzes the conversion of glutamic acid into gamma-amino butyric acid.  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
FEATURE 402-405 #domain DOPA decarboxylase binding #status predicted  
#label BIN  
SUMMARY #length 594 #molecular-weight 66894 #checksum 5491

Query Match 87.1%; Score 135; DB 2; Length 594;  
Best Local Similarity 75.0%; Pred. No. 1.57e-14;  
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGLDMVGLADM 204  
1 PRFNOLSTGLDMVGLADM 20

RESULT 15  
ENTRY A30999 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) C1 - fruit fly  
(Drosophila melanogaster)  
ALTERNATE\_NAMES L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Drosophila melanogaster  
DATE 26-Oct-1989 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999  
ACCESSIONS JH0192; PS0301; A30999  
REFERENCE JH0192  
#authors Jackson, F.R.; Newby, L.M.; Kulkarni, S.J.  
#journal J. Neurochem. (1990) 54:1068-1078  
#title Drosophila GABAergic systems: sequence and expression of

glutamic acid decarboxylase.  
#cross-references MUID:90155291  
#accession JH0192  
##molecule\_type mRNA  
##residues 1-510 #label JAC  
##cross-references GB:X76198; NID:q433082; PIDN:CA53791.1; PID:q433083  
#accession PS0301  
##molecule\_type mRNA  
##residues 156-200, 'F', 202-300, 'K', 302-384, 'L', 386-510 #label JAC  
COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

GENETICS #gene FlyBase:Gad1  
CLASSIFICATION #cross-references FlyBase:FBgn0004516  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate  
FEATURE 322 #binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted  
SUMMARY #length 510 #molecular-weight 57758 #checksum 3194

Query Match 74.2%; Score 115; DB 1; Length 510;  
Best Local Similarity 55.0%; Pred. No. 5.13e-10;  
Matches 11; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 102 PRFNOLSTGLDMVGLADM 121  
1 PRFNOLSTGLDMVGLADM 20

Search completed: Tue Mar 7 21:43:54 2000  
Job time : 8 secs.

\*\*\*\*\*  
 W O R L D  
 (TM)  
 \*\*\*\*\*

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Merch\_pp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Mar 7 21:41:36 2000; MasPar time 3.48 Seconds  
 Tabular output not generated. 171.624 Million cell updates/sec

Title: >US-08-981-824-5  
 Description: (1.20) From US08981824.pep  
 Perfect Score: 155  
 Sequence: 1 PRYFNUSTGLDMVGLADM 20

Scoring table: PAM 150  
 Gap 15

Searched: 82229/seqs, 29864866 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot38  
 1:swissprot

Statistics: Mean 30.945; Variance 41.805; scale 0.740

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	155	100.0	585	1	DCE2_RAT GLUTAMATE DECARBOXYLASE	2.36e+21
2	155	100.0	585	1	DCE2_PIG GLUTAMATE DECARBOXYLASE	2.36e+21
3	155	100.0	585	1	DCE2_HUMAN GLUTAMATE DECARBOXYLASE	2.36e+21
4	155	100.0	585	1	DCE2_MOUSE GLUTAMATE DECARBOXYLASE	2.36e+21
5	135	87.1	593	1	DCE1_MOUSE GLUTAMATE DECARBOXYLASE	3.19e+16
6	135	87.1	593	1	DCE1_RAT GLUTAMATE DECARBOXYLASE	3.19e+16
7	135	87.1	594	1	DCE1_PIG GLUTAMATE DECARBOXYLASE	3.19e+16
8	135	87.1	594	1	DCE1_HUMAN GLUTAMATE DECARBOXYLASE	3.19e+16
9	135	87.1	594	1	DCE1_FELCA GLUTAMATE DECARBOXYLASE	3.19e+16
10	115	74.2	510	1	DCE_DROME GLUTAMATE DECARBOXYLASE	2.68e+11
11	65	41.9	325	1	MURE_PSEAE UDP-N-ACETYLMURAMOYLAL	1.58e+00
12	65	41.9	325	1	AUTM_ARATH ASPARTATE AMINOTRANSFER	1.58e+00
13	62	40.0	344	1	MDH_METJA ASPARTATE AMINOTRANSFER	5.37e+00
14	62	40.0	405	1	AAT2_ARATH ASPARTATE AMINOTRANSFER	5.37e+00
15	62	40.0	407	1	AATC_ORISA ASPARTATE AMINOTRANSFER	5.37e+00
16	62	40.0	552	1	CHOD_BREST CHOLESTEROL OXIDASE PR	5.37e+00
17	61	39.4	360	1	HR38_BOMO PROBABLE NUCLEAR HOMO	7.98e+00
18	61	39.4	454	1	AATM_LUPAN ASPARTATE AMINOTRANSFER	7.98e+00
19	61	39.4	462	1	ALGC_PSEAE PHOSPHOMANNOMUTASE (EC	7.98e+00
20	61	39.4	538	1	YABK_HAEN HYPOTHETICAL PROTEIN H	7.98e+00
21	60	38.7	221	1	XGIX_HAEN PROBABLE TRANSCRIPTION	1.18e+01
22	60	38.7	251	1	C561_HUMAN CYTOCHROME B561 (CYTOC	1.18e+01
23	60	38.7	384	1	VANS_ENTFC SENSOR PROTEIN VANS (E	1.18e+01

RESULT	ID	1	STANDARD	PRT	585 AA.
AC	005683				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)				
DE	(65 KD GLUTAMIC ACID DECARBOXYLASE).				
GN	GAD5 OR GAD65				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Mammalia;				
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=HIPPOCAMPUS;				
RA	MEDLINE: 91299343.				
RA	ERLANDER M.G., TILAKARATNE N.J., FELDBLUM S., PATEL N.,				
RA	TOBIN A.J.;				
RT	"Two genes encode distinct glutamate decarboxylases.";				
RT	Neuron 7:91-100(1991).				
CC	-1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.				
CC	-1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).				
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE.				
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).				
CC	-1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE				
CC	DECARBOXYLASE.				
CC					
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CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>				
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
DR	EMBL: M72422; AAA63488.1;				
DR	PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.				
DR	PFAM: PF00282; pyridoxal_dec_1.				
KW	Neurotransmitter biosynthesis; Lyase; Decarboxylase;				
KW	pyridoxal phosphate; Multigene family.				
FT	BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).				
SEQUENCE	585 AA; 65402 MW; E35D601A CRC32;				

## ALIGNMENTS

Query Match 100.0%; Score 155; DB 1; Length 585;  
 Best local Similarity 100.0%; Pred. No. 2.36e+21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      176 PRYFNOLSTGLDMVGLADW 195
      |||||||
Oy      1 PRYFNOLSTGLDMVGLADW 20

RESULT  2
ID DCE2_PIG STANDARD: PRT: 585 AA.
AC P48321.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
CN GAD2 OR GAD65.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RA [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RX MEDLINE: 95137399.
RA SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
  "Sequences of two porcine glutamic acid decarboxylases (65- and
  67-kDa GAD).";
  RL Gene 152:257-260(1995).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
  TYDC).
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D31848; BAA06635.1; -.
CC PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal dec. 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
  KW pyridoxal phosphate; Multigene family.
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 585 AA: 65388 MW; F3E9BD88 CRC32;

Query Match 100.0%; Score 155; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 2,36e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      176 PRYFNOLSTGLDMVGLADW 195
      |||||||
Oy      1 PRYFNOLSTGLDMVGLADW 20

RESULT  3
ID DCE2_HUMAN STANDARD: PRT: 585 AA.
AC Q05329.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)
DE (65 KD GLUTAMIC ACID DECARBOXYLASE).
CN GAD2 OR GAD65.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RA [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 92196068.
RX BU D.-F., ERLANDER M.G., HITZ B.C., TILLAKARATNE N.J., KAUFMAN D.L.,

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RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;
  "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are
  each encoded by a single gene.";
  Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).
RA [2]
RP SEQUENCE FROM N.A.
RC MEDLINE: 94375018.
RX BU D.-F., TOBIN A.J.;
  "The exon-intron organization of the genes (GAD1 and GAD2) encoding
  two human glutamate decarboxylases (GAD67 and GAD65) suggests that
  they derive from a common ancestral GAD.";
  Genomics 21:222-228(1994).
RA [3]
RP SEQUENCE FROM N.A.
RC TISSUE-PANCREATIC ISLETS;
RX MEDLINE: 92020848.
RA KARLSEN A.E., HAGOPIAN W.A., GRUBIN C.E., DUBE S., DISTECHE C.M.,
  ADLER D.A., BARBEIER H., MATHWES S., GRANT F.J., FOSTER D.,
  LERNMARK A.;
  "Cloning and primary structure of a human islet isoform of glutamic
  acid decarboxylase from chromosome 10.";
  Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).
RA [4]
RP SEQUENCE OF 6-585 FROM N.A.
RC TISSUE-PANCREAS;
RX MEDLINE: 93185681.
RA MAUCH L., ABNEY C.C., BERG H., SCHERBAUM W.A., LIEVOGEL B.,
  NORTHEIMANN W.;
  "Characterization of a linear epitope within the human pancreatic
  64-kDa glutamic acid decarboxylase and its autoimmune recognition by
  sera from insulin-dependent diabetes mellitus patients.";
  Eur. J. Biochem. 212:597-603(1993).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE
  DECARBOXYLASE.
CC -----
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CC -----
CC EMBL: M81882; AAA62367.1; -.
CC EMBL: M74826; AAA58491.1; -.
CC EMBL: X69936; CAA49554.1; ALT-INIT.
DR EMBL: M70435; AAA52513.1; -.
DR PIR: A41292; A41292.
DR MIM: 138275; -.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal dec. 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
  KW pyridoxal phosphate; Multigene family.
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 585 AA: 65411 MW; BAD62B62 CRC32;

Query Match 100.0%; Score 155; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 2,36e-21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      176 PRYFNOLSTGLDMVGLADW 195
      |||||||
Oy      1 PRYFNOLSTGLDMVGLADW 20

RESULT  4
ID DCE2_MOUSE STANDARD: PRT: 585 AA.
AC P48320; Q35519;

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DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 DE (65 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD2 OR GAD65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE: 94032481.  
 RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;  
 RT "Cloning and sequence analysis of a murine cDNA encoding glutamate  
 RT decarboxylase (GAD65).";  
 RL Biochim. Biophys. Acta 1216:157-160(1993).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6; TISSUE-BRAIN;  
 RX MEDLINE: 97115675.  
 RA ASADA H., KAMAMURA Y., MARUYAMA K., KOME H., DING R.G., JI F.Y.,  
 RA KANBARA N., KUZUME H., SANBO M., YAGI T., OBARA K.;  
 RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase  
 RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but  
 RT are susceptible to seizures.";  
 RL Biochem. Biophys. Res. Commun. 229:891-895(1996).  
 RN [3]  
 RN SEQUENCE OF 175-379 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localization and quantitation of expression of two glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat.";  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 CC DECARBOXYLASE.  
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 CC -----  
 CC EMBL: L16980; AAA93049.1; -  
 CC EMBL: DA2051; BAA22893.1; -  
 CC EMBL: S67454; CAB32806.1; -  
 CC MGD: MGI:95634; GAD2.  
 CC PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 CC PFM: PF00282; Pyridoxal\_dec; 1.  
 CC Neurotransmitter biosynthesis: Lyase: Decarboxylase;  
 CC Pyridoxal phosphate: Multigene family.  
 CC BINDING 396  
 CC FT CONFLICT 259 259 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 CC FT CONFLICT 319 319 I -> S (IN REF. 2).  
 CC FT CONFLICT 325 325 K -> E (IN REF. 2).  
 CC FT CONFLICT 499 499 P -> S (IN REF. 2).  
 CC SEQUENCE 585 AA; 65224 MW; 9B5C088 CRC32;  
 SO  
 Query Match 100.0%; Score 155; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 2,36e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 176 PRYFNOLSTGLDNGLAADW 195  
 ||||||||||||||||  
 QY 1 PRYFNOLSTGLDNGLAADW 20

RESULT 5  
 ID DEEL\_MOUSE STANDARD; PRT; 593 AA.  
 AC P48318;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA KATAROVA Z., SZABO G., MUGNANI E., GREENSPAN R.;  
 RT "Molecular identification of the 62 kd form of glutamic acid  
 RT decarboxylase from the mouse.";  
 RL Eur. J. Neurosci. 2:190-202(1990).  
 RN [2]  
 RN SEQUENCE OF 198-403 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., GRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localization and quantitation of expression of two glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat.";  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
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 CC -----  
 CC EMBL: 249976; CA50207.1; -  
 CC EMBL: S67453; CAB32805.1; -  
 CC MGD: MGI:95632; GAD1.  
 CC PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 CC PFM: PF00282; Pyridoxal\_dec; 1.  
 CC Neurotransmitter biosynthesis: Lyase: Decarboxylase;  
 CC Pyridoxal phosphate: Multigene family.  
 CC BINDING 404  
 CC FT CONFLICT 234 234 E -> K (IN REF. 2).  
 CC FT CONFLICT 258 258 S -> T (IN REF. 1).  
 CC FT CONFLICT 360 360 D -> S (IN REF. 1).  
 CC SEQUENCE 593 AA; 66584 MW; 63BC57AA CRC32;  
 SO  
 Query Match 87.1%; Score 135; DB 1; Length 593;  
 Best Local Similarity 75.0%; Pred. No. 3,19e-16;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 Db 184 PRYFNOLSTGLDNGLAADW 203  
 ||||||||||||||||  
 QY 1 PRYFNOLSTGLDNGLAADW 20  
 RESULT 6  
 ID DEEL\_RAT STANDARD; PRT; 593 AA.  
 AC P18088;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)

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DE  GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE  (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN  GAD1 OR GAD67.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC  Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE: 91014554.
RA  WYBORSKI R.J., BOND R.W., GOTTLIEB D.I.;
RT  "Characterization of a cDNA coding for rat glutamic acid
RT  decarboxylase."
RL  Brain Res. Mol. Brain Res. 8:193-198(1990).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE: 90132703.
RA  JULIEN J.F., SAMAMA P., MALLET J.;
RT  "Rat brain glutamic acid decarboxylase sequence deduced from a cloned
RT  cDNA."
RL  J. Neurochem. 54:703-705(1990).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE: 92020930.
RA  MICHELSEN B.K., PETERSEN J.S., BOEL E., MOLDROP A., DYBERG T.,
RA  MADSEN O.D.;
RT  "Cloning, characterization, and autoimmune recognition of rat islet
RT  glutamic acid decarboxylase in insulin-dependent diabetes mellitus."
RL  Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
CC  -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC  -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC  -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC  -1- SUBUNIT: HOMODIMER.
CC  -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC  TYRDC).
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: M34445; AAC42037.1; -
DR  EMBL: X57572; CAA40800.1; -
DR  EMBL: X57573; CAA40801.1; -
DR  EMBL: M76177; AAA41184.1; -
DR  PIR: A41367; A41367.
DR  PIR: A43756; A43756.
DR  PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR  PFAM: PF00282; pyridoxal_dec; 1.
KW  Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW  pyridoxal phosphate; Multigene family.
FT  BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT  CONFLICT 103 103 L -> V (IN REF. 2).
FT  CONFLICT 284 284 F -> S (IN REF. 2).
FT  CONFLICT 287 288 EH -> AD (IN REF. 2).
FT  CONFLICT 344 345 AG -> EA (IN REF. 2).
FT  CONFLICT 347 347 T -> I (IN REF. 2).
FT  CONFLICT 352 353 FD -> LE (IN REF. 2).
FT  CONFLICT 380 380 L -> R (IN REF. 2).
SQ  SEQUENCE 593 AA: 66640 MW: 5A0B67C0 CRC32;

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Query Match 87.1%; Score 135; DB 1; Length 593;  
 Best Local Similarity 75.0%; Pred. No. 3.19e-16;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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DB  184 PRFENQSTGLDITGLAGEM 203
OY  1 PRFENQSTGLDMVGLADW 20

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RESULT 7

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ID  DCEL_PIG STANDARD; PRT: 594 AA.
AC  P48319.
DT  01-FEB-1996 (Rel. 33, Created)
DT  01-FEB-1996 (Rel. 33, Last sequence update)
DT  01-FEB-1996 (Rel. 33, Last annotation update)
DE  GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE  (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN  GAD1 OR GAD67.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC  Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  TISSUE-BRAIN.
RX  MEDLINE: 95137399.
RA  SUZUKI R., ASAMI N., AMANN E., WAGATSUNA M.;
RT  "Sequences of two porcine glutamic acid decarboxylases (65- and
RT  67-kDa GAD)."
RL  Gene 152:257-260(1995).
CC  -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC  -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC  -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC  TYRDC).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: D31849; BAA06636.1; -
DR  PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR  PFAM: PF00282; pyridoxal_dec; 1.
KW  Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW  pyridoxal phosphate; Multigene family.
FT  BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT  PIR: A405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ  SEQUENCE 594 AA: 66894 MW: 69D6C79C CRC32;

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Query Match 87.1%; Score 135; DB 1; Length 594;  
 Best Local Similarity 75.0%; Pred. No. 3.19e-16;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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DB  185 PRFENQSTGLDITGLAGEM 204
OY  1 PRFENQSTGLDMVGLADW 20

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RESULT 8
ID  DCEL_HUMAN STANDARD; PRT: 594 AA.
AC  O99259.
DT  01-FEB-1996 (Rel. 33, Created)
DT  01-FEB-1996 (Rel. 33, Last sequence update)
DT  01-FEB-1996 (Rel. 34, Last annotation update)
DE  GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE  (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN  GAD1 OR GAD.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC  Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  TISSUE-BRAIN.
RX  MEDLINE: 92196068.
RA  BU D.-F., ERLANDER M.G., HITZ B.C., TILAKARATNE N.J., KAUFMAN D.L.,
RA  WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;
RT  "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are
RT  each encoded by a single gene."
RL  Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).
RN  [2]

```



RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94375018.  
 RA BU D.-F., TOBIN A.J.;  
 RT "The exon-intron organization of the genes (GAD1 and GAD2) encoding  
 RT two human glutamate decarboxylases (GAD67 and GAD65) suggests that  
 RT they derive from a common ancestral GAD.";  
 RL Genomics 21:222-228(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 93080286.  
 RA KELLY C.D., EDWARDS Y., JOHNSTONE A.P., HARFEST E., NOGRADI A.,  
 RA NUSSEY S.S., POVEY S., CARTER N.D.;  
 RT "Nucleotide sequence and chromosomal assignment of a cDNA encoding  
 RT the large isoform of human glutamate decarboxylase.";  
 RL Ann. Hum. Genet. 56:255-265(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 93282844.  
 RA YAMASHITA K., CRAM D.S., HARRISON L.C.;  
 RT "Molecular cloning of full-length glutamic acid decarboxylase 67 from  
 RT human pancreas and islets.";  
 RL Biochem. Biophys. Res. Commun. 192:1347-1352(1993).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PANCREATIC ISLETS;  
 RX MEDLINE: 93282845.  
 RA KAMASAKI E., MORIUCHI R., WATANABE M., SATOH K., BRUNICARDI F.C.,  
 RA KAITI P.C., YAMAGUCHI T., MULLEN Y., AKAZAWA S., MIYAMOTO T.;  
 RT "Cloning and expression of large isoform of glutamic acid  
 RT decarboxylase from human pancreatic islet.";  
 RL Biochem. Biophys. Res. Commun. 192:1353-1359(1993).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RA GIORDA R., PEAKMAN M., VERGANI D., TRUCCO M.;  
 RT Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.  
 RL [7]  
 RP SEQUENCE OF 218-397 FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 91248209.  
 RA CRAM D.S., BARRETT L.D., JOSEPH J.L., HARRISON L.C.;  
 RT "Cloning and partial nucleotide sequence of human glutamic acid  
 RT decarboxylase cDNA from brain and pancreatic islets.";  
 RL Biochem. Biophys. Res. Commun. 176:1239-1244(1991).  
 RN [8]  
 RP SEQUENCE OF 527-594 FROM N.A.  
 RC TISSUE-TESTIS;  
 RX MEDLINE: 90355986.  
 RA PERSSON H., PELTO-HUIKKO M., METSIS M., SOEDER O., BRENE S.,  
 RA SKOG S., HOEKFELT T., RITZEN E.M.;  
 RT "Expression of the neurotransmitter-synthesizing enzyme glutamic acid  
 RT decarboxylase in male germ cells.";  
 RL Mol. Cell. Biol. 10:4701-4711(1990).  
 CC [1]- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC [1]- CATALYTIC ACTIVITY: L-GLUTAMATE + CO(2).  
 CC [1]- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC [1]- SUBUNIT: HOMODIMER.  
 CC [1]- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
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 CC -----  
 CC EMBL: M81883: AAA62368.1: -  
 CC EMBL: L16888: AAB59427.1: -  
 CC EMBL: 222750: CAAB0435.1: -  
 CC EMBL: S61897: AAB26937.1: -  
 CC EMBL: S61898: AAB26938.1: -

DR EMBL: M86522: AAA35900.1: -  
 DR EMBL: M70434: AAA52512.1: -  
 DR EMBL: M55574: AAA72938.1: -  
 DR EMBL: A28074: CAAB0435.1: -  
 DR PIR: P00157: P00157.  
 DR MIM: 266100: -  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 FT CONFLICT 9 9 MISSING (IN REF. 6).  
 FT CONFLICT 16 17 GA -> EP (IN REF. 3).  
 FT CONFLICT 17 17 A -> Q (IN REF. 6).  
 FT CONFLICT 18 18 D -> N (IN REF. 5).  
 FT CONFLICT 31 31 T -> N (IN REF. 5).  
 FT CONFLICT 68 68 K -> R (IN REF. 1 AND 2).  
 FT CONFLICT 116 116 F -> L (IN REF. 5).  
 FT CONFLICT 136 136 T -> A (IN REF. 6).  
 FT CONFLICT 140 140 D -> E (IN REF. 6).  
 FT CONFLICT 142 142 H -> R (IN REF. 6).  
 FT CONFLICT 155 155 N -> T (IN REF. 5).  
 FT CONFLICT 206 206 T -> N (IN REF. 3).  
 FT CONFLICT 302 302 G -> C (IN REF. 5).  
 FT CONFLICT 436 436 F -> L (IN REF. 4).  
 FT CONFLICT 512 512 N -> S (IN REF. 4).  
 FT CONFLICT 477 477 E -> G (IN REF. 5).  
 FT CONFLICT 492 492 A -> G (IN REF. 5).  
 FT CONFLICT 565 565 F -> L (IN REF. 3).  
 SQ SEQUENCE 594 AA: 66896 MW: 94733552 CRC32:

Query Match 87.1%; Score 135; DB 1; Length 594;  
 Best Local Similarity 75.0%; Pred. No. 3,19e-16;  
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 Db 185 PRFNOLSTGLDITGLAGEW 204  
 QY 1 PRYFNOLSTGLDITGLAGEW 20  
 ID DEEL\_FELCA STANDARD; PRT; 594 AA.  
 AC P14748;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-OCIPITAL CORTEX;  
 RX MEDLINE: 87310623.  
 RA KOBAYASHI Y., KAUFMAN D.L., TOBIN A.J.;  
 RT "Glutamic acid decarboxylase cDNA: nucleotide sequence encoding an  
 RT enzymatically active fusion protein.";  
 RL J. Neurosci. 7:2768-2772(1987).  
 CC [1]- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC [1]- CATALYTIC ACTIVITY: L-GLUTAMATE + CO(2).  
 CC [1]- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC [1]- SUBUNIT: HOMODIMER.  
 CC [1]- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
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CC -----
DR EMBL: M18629; AAS1430.1; -
DR PIR: A45671; A45671.
DR PIR: A46758; A46758.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal_dec; 1.
DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multiligene family.
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 594 AA; 66824 MW; 3EC20778 CRC32;

Query Match 87.1%; Score 135; DB 1; Length 594;
Best Local Similarity 75.0%; Pred. No. 3.19e-16;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 185 PRFNOLSTGLDMLGADW 204
1 PRFNOLSTGLDMLGADW 20

RESULT 10
ID DCE_DROME STANDARD: PRT; 510 AA.
AC P20228;
DT 01-FEB-1991 (Rel. 17, Created)
NM 01-FEB-1991 (Rel. 17, Last sequence update)
NT 01-NOV-1995 (Rel. 32, Last annotation update)
DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).
GN GAD OR GLB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Ephydrogata; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 90155291.
RA JACKSON F.R., NEMBY L.M., KULKARNI S.J.;
RT "Drosophila GABAergic systems: sequence and expression of glutamic
RT acid decarboxylase".
RL J. Neurochem. 54:1068-1078(1990).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE -> 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
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CC -----
CC EMBL: X76198; CAAS3791.1; -
CC PIR: A30999; A30999.
CC PIR: JH0192; JH0192.
CC FLYBASE: FBgn0004516; Gad1.
CC PROSITE: PS00392; DDC_GAD_HDC_YDC; 1.
CC PFAM: PF00282; pyridoxal_dec; 1.
CC Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate.
FT BINDING 322 322 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 510 AA; 57758 MW; 97C7A8F1 CRC32;

Query Match 74.2%; Score 115; DB 1; Length 510;
Best Local Similarity 55.0%; Pred. No. 2.68e-11;
Matches 11; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Db 102 PRFNOLSTGLDMLGADW 121
1 PRFNOLSTGLDMLGADW 20

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RESULT 11
ID MURE_PSEAE STANDARD: PRT; 325 AA.
AC 059650;
DT 01-NOV-1997 (Rel. 35, Created)
NM 01-NOV-1997 (Rel. 35, Last sequence update)
NT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UDP-N-ACETYLURAMIDYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE
DE (EC 6.3.2.13) (UDP-N-ACETYLURAMYL-TRIPETIDE SYNTHETASE) (MESO-
DE DIMINOPIMELATE-ADDING ENZYME) (FRAGMENT).
GN MURE.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
OC [1]
RN SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PAOI;
RX MEDLINE: 96100768.
RA LIAO X., HANCOCK R.E.W.;
RT "Cloning and characterization of the Pseudomonas aeruginosa pbpb gene
RT encoding penicillin-binding protein 3.".
RL Antimicrob. Agents Chemother. 39:1871-1874(1995).
CC -1- FUNCTION: CELL WALL FORMATION. DIAMINOPIMELIC ACID ADDING ENZYME.
CC -1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLURAMOTL-L-ALANYL-D-
CC GLUTAMATE + MESO-2,6-DIAMINOPIMELIDIC ACID -> ADP + ORTHOPHOSPHATE
CC + UDP-N-ACETYLURAMOTL-L-ALANYL-D-GLUTAMYL-MESO-2,6-
CC DIAMINOPIMELIDIC ACID.
CC -1- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE MURCEP FAMILY.
CC -----
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CC -----
CC EMBL: X84053; CAAS8873.1; -
CC PIR: PF01225; Mur_Ligase; 1.
CC PFAM: PF01225; Mur_Ligase; 1.
CC Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
KW ATP-binding.
KW NP_BIND 108 114 ATP (POTENTIAL).
FT NON_TER 325 325
FT SEQUENCE 325 AA; 34215 MW; 442CD550 CRC32;

Query Match 41.9%; Score 65; DB 1; Length 325;
Best Local Similarity 35.3%; Pred. No. 1.56e+00;
Matches 6; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Db 92 RYFGEPSRGLDMLGADW 108
2 RYFGEPSRGLDMLGADW 18

RESULT 12
ID AATM_ARATH STANDARD: PRT; 453 AA.
AC P46248;
DT 01-NOV-1995 (Rel. 32, Created)
NM 01-NOV-1995 (Rel. 32, Last sequence update)
NT 01-NOV-1995 (Rel. 35, Last annotation update)
DE ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (EC 2.6.1.1)
DE (TRANSMINASE A).
GN AAT1 OR ASP5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE-LEAF;  
 RA WILKIE S.E., ROPER J., SMITH A., WARREN M.J.;  
 RN Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RA SEQUENCE FROM N.A.  
 RC STRAIN-CV. LANDSBERG ERECTA; TISSUE-LEAF;  
 RA WILKIE S.E., LAMBERT R., WARREN M.J.;  
 RN Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-  
 CC CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN  
 CC METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.  
 CC -1- CATALYTIC ACTIVITY: L-ASPARATE + 2-OXOGUTARATE -> OXALACETATE +  
 CC L-GLUTAMATE.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
 CC -----  
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 CC -----  
 CC EMBL: X81026; CAA56932.1; -  
 CC EMBL: X91865; CAA62972.1; -  
 CC DR HSSP: P00508; 1TAT  
 CC DR PROSITE: P500105; AA-TRANSFER-CLASS\_1; 1.  
 CC DR PFAM: PF00155; aminotran\_1; 1.  
 CC DR TRANSFERASE: Aminotransferase; Pyridoxal phosphate; Mitochondrion;  
 CC KM Transit peptide: Multigene family.  
 CC FT TRANSIT 1 52 MITOCHONDRION (POTENTIAL).  
 CC FT CHAIN 53 453 ASPARTATE AMINOTRANSFERASE.  
 CC FT BINDING 298 298 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC SQ SEQUENCE 453 AA; 49803 MW; 0B0381EA CRC32;  
 CC -----  
 CC Query Match 41.9%; Score 65; DB 1; Length 453;  
 CC Best Local Similarity 44.4%; Pred. NO. 1.58e+00;  
 CC Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 CC Db 199 RYDPTKIGLDFEGMAD 216  
 CC |||: ||| |:  
 CC QY 2 RYFNLSTGLDMVGLAD 19  
 CC -----  
 CC RESULT 13  
 CC ID MGH\_METJA STANDARD; PRT; 344 AA.  
 CC AC 058820;  
 CC DT 01-NOV-1997 (Rel. 35, Created)  
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 CC DE MALATE DEHYDROGENASE (EC 1.1.1.37) (EC 1.1.1.82).  
 CC GN MGH OR M1425.  
 CC OS Methanococcus jannaschii.  
 CC OC Archaea: Euryarchaeota: Methanococcales: Methanococcaceae;  
 CC OC Methanococcus.  
 CC RA KLENK H.-P., FRASER C.M., SMITH H.O., MOESE C.R., VENTER J.C.;  
 CC "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 CC jannaschii".

RL Science 273:1058-1073(1996).  
 CC -1- CATALYTIC ACTIVITY: L-MALATE + NAD(+) -> OXALACETATE + NADH.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE "ARCHAEBACTERIAL" MALATE DEHYDROGENASE  
 CC FAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL: U67583; AAB99436.1; -  
 CC DR TIGR: M01425; -  
 CC KM Oxidoreductase: Tricarboxylic acid cycle; NAD.  
 CC FT ACT\_SITE 186 186 PROTON-RELAY (POTENTIAL).  
 CC FT BINDING 189 189 SUBSTRATE CARBOXYL GROUP (POTENTIAL).  
 CC SQ SEQUENCE 344 AA; 37358 MW; 457C3727 CRC32;  
 CC -----  
 CC Query Match 40.0%; Score 62; DB 1; Length 344;  
 CC Best Local Similarity 33.3%; Pred. NO. 5.37e+00;  
 CC Matches 5; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 CC Db 122 YSELANODMIGIT 136  
 CC |||: |||:  
 CC QY 3 YFNQSTGLDMVGLA 17  
 CC -----  
 CC RESULT 14  
 CC ID AAT2\_AATH STANDARD; PRT; 405 AA.  
 CC AC P46645;  
 CC DT 01-NOV-1995 (Rel. 32, Created)  
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 CC DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 CC DE ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISOZYME 1 (EC 2.6.1.1)  
 CC DE (TRANSAMINASE A).  
 CC GN ASP2.  
 CC OS Arabidopsis thaliana (Mouse-ear cress).  
 CC OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;  
 CC OC euphyllophytes: Spermatophyta: Magnoliophyta: eudicotyledons;  
 CC OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
 CC OC Arabidopsis.  
 CC RA SCHULTZ C.J., CORUZZI G.M.;  
 CC "The aspartate aminotransferase gene family of Arabidopsis encodes  
 CC RT isoenzymes localized to three distinct subcellular compartments.";  
 CC RN Plant J. 7:61-75(1995).  
 CC [2]  
 CC RP SEQUENCE OF 327-405 FROM N.A.  
 CC RC STRAIN-CV. COLUMBIA; TISSUE-LEAF;  
 CC RX MEDLINE: 95201829.  
 CC RA SCHULTZ C.J., CORUZZI G.M.;  
 CC "The aspartate aminotransferase gene family of Arabidopsis encodes  
 CC RT isoenzymes localized to three distinct subcellular compartments.";  
 CC RN Plant J. 7:61-75(1995).  
 CC [2]  
 CC RP SEQUENCE OF 327-405 FROM N.A.  
 CC RC STRAIN-CV. COLUMBIA; TISSUE-LEAF;  
 CC RA PARMENTIER Y., CRIQUI M.C., DURR A., FLECK J.;  
 CC Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.  
 CC CC -1- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-  
 CC CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN  
 CC METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.  
 CC -1- CATALYTIC ACTIVITY: L-ASPARATE + 2-OXOGUTARATE -> OXALACETATE +  
 CC L-GLUTAMATE.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
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DR EMBL: U15033: AAA79370.1: -

DR EMBL: 226740: CAA8141.1: -

DR HSSP: P00508: ITAT.

DR PROSITE: PS00105: AA\_TRANSFERR\_CLASS\_1: 1.

DR PFAM: PF00155: aminotran\_1: 1.

KW Transferase: Aminotransferase; Pyridoxal phosphate; Multigene family.

FT BINDING 251 251 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SEQUENCE 405 AA: 44296 MW: A1D4EBF5 CRC32:

Db 152 RYDPATRGIDFGLLED 169

QY 2 RYFNOLSTGLDMVGLAAD 19

Query Match 40.0%; Score 62; DB 1; Length 405;

Best Local Similarity 44.4%; Pred. No. 5.37e+00;

Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

RESULT 15

ID AATC\_ORYSA STANDARD; PRT; 407 AA.

AC P37833:

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (EC 2.6.1.1) (TRANSAMINASE A).

OS Oryza sativa (Rice).

OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;

OC euphyllophytes: Spermatophyta: Magnoliophyta: Liliopsida: Poales;

OC Poaceae: Oryza.

RM [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RX MEDLINE: 97191542.

RA SONG J., SASAKI T., MINOBE Y.;

RT "Characterization and mapping of cDNA encoding aspartate

amino transferase in rice, Oryza sativa L.";

RT DNA Res. 3:303-310(1996).

CC -!- FUNCTION: IMPORTANT FOR THE METABOLISM OF AMINO ACIDS AND KREBS-

CYCLE RELATED ORGANIC ACIDS. IN PLANTS, IT IS INVOLVED IN NITROGEN

METABOLISM AND IN ASPECTS OF CARBON AND ENERGY METABOLISM.

CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +

L-GLUTAMATE.

CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT

AMINOTRANSFERASES.

CC -----

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CC -----

DR EMBL: D14673: BAA03504.1: -

DR HSSP: P00508: ITAT.

DR PROSITE: PS00105: AA\_TRANSFERR\_CLASS\_1: 1.

DR PFAM: PF00155: aminotran\_1: 1.

KW Transferase: Aminotransferase; Pyridoxal phosphate.

FT BINDING 253 253 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SEQUENCE 407 AA: 44507 MW: E5DC8A40 CRC32:

Query Match 40.0%; Score 62; DB 1; Length 407;

Best Local Similarity 44.4%; Pred. No. 5.37e+00;

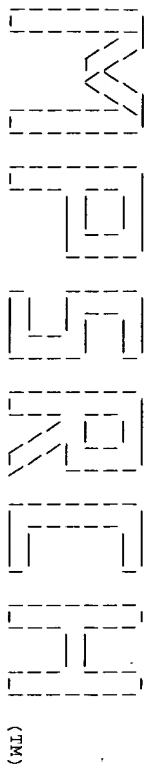
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Db 154 RYDPATRGIDFGLLED 171

QY 2 RYFNOLSTGLDMVGLAAD 19

QY 2 RYFNOLSTGLDMVGLAAD 19

Search completed: Tue Mar 7 21:41:43 2000  
Job time : 7 secs.



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Mperch\_pp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:43:15 2000; MasPar time 9.40 Seconds  
147.588 Million cell updates/sec  
Tabular output not generated.

Title: >US-08-981-824-5  
Description: (1-20) from US08981824.pep  
Perfect Score: 155  
Sequence: 1 PRYFNOLSTGLDMVGLADW 20

Scoring table: PAM 150  
Gap 15

Searched: 225878 seqs, 69334122 residues  
Post-processing: Minimum Match 0%  
Lifting first 45 summaries

Database: spiremb12  
1:sp\_archaea 2:sp\_bacteria 3:sp\_fungi 4:sp\_human  
5:sp\_invertebrate/6:sp\_mammal 7:sp\_mhc 8:sp\_organelle  
9:sp\_phage 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified  
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 29.883; Variance 41.692; scale 0.717

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	144	92.9	590 13	O9Y158	GLUTAMATE DECARBOXYLASE	6.38e-18
2	135	87.1	223 11	O63211	GLUTAMATE DECARBOXYLASE	1.10e-15
3	135	87.1	593 11	O08685	67KD GLUTAMIC ACID DEC	1.10e-15
4	115	74.2	370 5	O44102	GLUTAMIC ACID DECARBOX	7.32e-11
5	115	74.2	370 5	O44103	GLUTAMIC ACID DECARBOX	7.32e-11
6	114	73.5	508 5	O9XTP4	GLUTAMIC ACID DECARBOX	1.26e-10
7	80	51.6	78 11	P70713	CYSTEINE SULFINATE DEC	4.03e-03
8	80	51.6	267 4	O9Y602	CYSTEINE SULFINIC ACID	4.03e-03
9	80	51.6	478 11	O64577	CYSTEINE SULFINIC ACID	4.03e-03
10	80	51.6	493 4	O9Y600	CYSTEINE SULFINIC ACID	4.03e-03
11	80	51.6	493 11	O64611	CYSTEINE SULFINATE DEC	4.03e-03
12	73	47.1	387 5	O17621	C29F7.2 PROTEIN.	9.85e-02
13	71	45.8	394 5	O17620	C29F7.1 PROTEIN.	2.38e-01
14	68	43.9	192 2	P94758	RIBOKINASE (EC 2.7.1.1	8.70e-01
15	67	43.2	169 2	O52961	ORF14.	1.33e+00
16	67	43.2	673 14	O89816	ENVELOPE GLYCOPROTEIN.	1.33e+00
17	65	41.9	370 1	O9YER2	370AA LONG HYDROPHETIC	3.07e+00
18	65	41.9	378 10	O24459	DELTA-12 OLEATE DESATUR	3.07e+00
19	65	41.9	412 2	O9Z1H8	CP52K	3.07e+00
20	65	41.9	453 10	O49392	ASPARTATE AMINOTRANSFE	3.07e+00

RESULT ID	Query Match	Score	Length	DB ID	Description	Pred. No.
1	144	92.9	590 13	O9Y158	GLUTAMATE DECARBOXYLASE	6.38e-18
2	135	87.1	223 11	O63211	GLUTAMATE DECARBOXYLASE	1.10e-15
3	135	87.1	593 11	O08685	67KD GLUTAMIC ACID DEC	1.10e-15
4	115	74.2	370 5	O44102	GLUTAMIC ACID DECARBOX	7.32e-11
5	115	74.2	370 5	O44103	GLUTAMIC ACID DECARBOX	7.32e-11
6	114	73.5	508 5	O9XTP4	GLUTAMIC ACID DECARBOX	1.26e-10
7	80	51.6	78 11	P70713	CYSTEINE SULFINATE DEC	4.03e-03
8	80	51.6	267 4	O9Y602	CYSTEINE SULFINIC ACID	4.03e-03
9	80	51.6	478 11	O64577	CYSTEINE SULFINIC ACID	4.03e-03
10	80	51.6	493 4	O9Y600	CYSTEINE SULFINIC ACID	4.03e-03
11	80	51.6	493 11	O64611	CYSTEINE SULFINATE DEC	4.03e-03
12	73	47.1	387 5	O17621	C29F7.2 PROTEIN.	9.85e-02
13	71	45.8	394 5	O17620	C29F7.1 PROTEIN.	2.38e-01
14	68	43.9	192 2	P94758	RIBOKINASE (EC 2.7.1.1	8.70e-01
15	67	43.2	169 2	O52961	ORF14.	1.33e+00
16	67	43.2	673 14	O89816	ENVELOPE GLYCOPROTEIN.	1.33e+00
17	65	41.9	370 1	O9YER2	370AA LONG HYDROPHETIC	3.07e+00
18	65	41.9	378 10	O24459	DELTA-12 OLEATE DESATUR	3.07e+00
19	65	41.9	412 2	O9Z1H8	CP52K	3.07e+00
20	65	41.9	453 10	O49392	ASPARTATE AMINOTRANSFE	3.07e+00

ALIGNMENTS

RESULT ID	Query Match	Score	Length	DB ID	Description	Pred. No.
1	144	92.9	590 13	O9Y158	GLUTAMATE DECARBOXYLASE	6.38e-18
2	135	87.1	223 11	O63211	GLUTAMATE DECARBOXYLASE	1.10e-15
3	135	87.1	593 11	O08685	67KD GLUTAMIC ACID DEC	1.10e-15
4	115	74.2	370 5	O44102	GLUTAMIC ACID DECARBOX	7.32e-11
5	115	74.2	370 5	O44103	GLUTAMIC ACID DECARBOX	7.32e-11
6	114	73.5	508 5	O9XTP4	GLUTAMIC ACID DECARBOX	1.26e-10
7	80	51.6	78 11	P70713	CYSTEINE SULFINATE DEC	4.03e-03
8	80	51.6	267 4	O9Y602	CYSTEINE SULFINIC ACID	4.03e-03
9	80	51.6	478 11	O64577	CYSTEINE SULFINIC ACID	4.03e-03
10	80	51.6	493 4	O9Y600	CYSTEINE SULFINIC ACID	4.03e-03
11	80	51.6	493 11	O64611	CYSTEINE SULFINATE DEC	4.03e-03
12	73	47.1	387 5	O17621	C29F7.2 PROTEIN.	9.85e-02
13	71	45.8	394 5	O17620	C29F7.1 PROTEIN.	2.38e-01
14	68	43.9	192 2	P94758	RIBOKINASE (EC 2.7.1.1	8.70e-01
15	67	43.2	169 2	O52961	ORF14.	1.33e+00
16	67	43.2	673 14	O89816	ENVELOPE GLYCOPROTEIN.	1.33e+00
17	65	41.9	370 1	O9YER2	370AA LONG HYDROPHETIC	3.07e+00
18	65	41.9	378 10	O24459	DELTA-12 OLEATE DESATUR	3.07e+00
19	65	41.9	412 2	O9Z1H8	CP52K	3.07e+00
20	65	41.9	453 10	O49392	ASPARTATE AMINOTRANSFE	3.07e+00

```

RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 91062362.
RA      BOND R.W., WBOBRSKI R.J., GORTLIER D.I.;
RT      "Developmentally regulated expression of an exon containing a stop
RC      codon in the gene for glutamic acid decarboxylase."
RL      Proc. Natl. Acad. Sci. U.S.A. 87:8771-8775(1990).
DR      EMBL; M38350; AAA4185.1; -.
PR      PFM: PF00282; pyridoxal_dec; 1.
SQ      SEQUENCE 223 AA; 25069 MW; C7162AC1 CRC32;

Query Match          87.1%; Score 135; DB 11; Length 223;
Best Local Similarity 75.0%; Pred. No. 1,10e-15;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Db 184 PRFNOLSTGLDITGLAGEW 203
   |||||||||:::|||
Oy 1 PRYFNOJSTGLDMVGLADW 20

RESULT 3
ID 008685 PRELIMINARY; PRT; 593 AA.
AC 008685;
DT 01-JUL-1997 (TREMBLrel_04, Created)
DT 01-JUN-1997 (TREMBLrel_04, Last sequence update)
DT 01-NOV-1999 (TREMBLrel_12, Last annotation update)
DE 67KD GLUTAMIC ACID DECARBOXYLASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
NC Eutheria; Rodentia; Sciurognath; Muridae; Murine; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA AJST G., STEINBERNER H., THAMM B., ROST A.K., SEISSER J.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
DR EMBL; Y12257; CAAT2934.1; -.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFM: PF00282; pyridoxal_dec; 1.
KW lase; Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 593 AA; 66648 MW; BAFF92E0 CRC32;

Query Match          87.1%; Score 135; DB 11; Length 593;
Best Local Similarity 75.0%; Pred. No. 1,10e-15;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 184 PRFNOLSTGLDITGLAGEW 203
   |||||||||:::|||
Oy 1 PRYFNOJSTGLDMVGLADW 20

RESULT 4
ID 044102 PRELIMINARY; PRT; 370 AA.
AC 044102;
DT 01-JUN-1998 (TREMBLrel_06, Created)
DT 01-JUN-1998 (TREMBLrel_06, Last sequence update)
DT 01-NOV-1999 (TREMBLrel_12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).
GN GAD1.
OS Eusarchaea pseudoscutura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Phlebotomina; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Empidoidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RA ZENG L.-W., COMERON J.M., CHEN B., KREITMAN M.;
RL Genetica 0:0-0(1997).
DR EMBL; AF025807; AAB87892.1; -.
DR HSSP; P06543; 100d
DR FLTBAS; FBgm0023295; Dpse\Gad1.
PR PFM: PF00282; pyridoxal_dec; 2.

```

FT	NON TER	1		1	
SO	SEQUENCE	370 AA;	41887 MW;	A1E9456F CRC32;	
 Query Match					
		Best Local Similarity	55.0%;	Pred. No.	7.32e-11;
		Matches	11; Conservative	Mismatches	1; Indels
				0; Gaps	0;
 Db					
		22 PHFNOLSTGDLNVLADW 41			
		1 PRYENOLSTGDLNVLADW 20			
 RESULT					
ID	044103	PRELIMINARY;	PRT;	370 AA.	
AC	044103;				
DT	01-JUN-1998 (TREMBLrel. 06, Created)				
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).				
GN	GADI.				
OS	Drosophila subobscura (Fruit fly).				
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;				
CC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
CC	Ephydroidea; Drosophilidae; Drosophila.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	ZENG L.-M., COMERON J. M., CHEN B., KREITMAN M.;				
RL	Genetica 0:0-0(1997).				
DR	EMBL; AF025808; AAB87693.1; -.				
DR	HSSP; P06543; 100C.				
DR	FLYBASE; FBgn0023244; Dsub\Gadi.				
DR	PFAM; PF00282; pyridoxal_dec; 2.				
FT	NON TER	1			
FT	NON TER	370			
SO	SEQUENCE	370 AA;	41923 MW;	D75BDC49 CRC32;	
 Query Match					
		Best Local Similarity	74.2%;	Score	115; DB
		Matches	11; Conservative	Pred. No.	7.32e-11;
				Mismatches	1; Indels
				0; Gaps	0;
 Db					
		22 PHFNOLSTGDLNVLADW 41			
		1 PRYENOLSTGDLNVLADW 20			
 RESULT					
ID	09XTP4	PRELIMINARY;	PRT;	508 AA.	
AC	09XTP4;				
DT	01-NOV-1999 (TREMBLrel. 12, Created)				
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	GLUTAMIC ACID DECARBOXYLASE.				
GN	UNC-25 OR Y17D8A.23.				
OS	Cenorhabditis elegans.				
OC	Eukaryota; Metacoa; Nematoda; Secernentea; Rhabditiia; Rhabditida;				
CC	Rhabditiina; Rhabditoidea; Rhabditidae; Peloderiinae; Caenorhabditis.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BRISTOL;				
RX	MEDLINE; 99098940.				
RA	JIN Y., JORGENSEN E., HARTWIG E., HORVITZ H.R.;				
RT	"The Cenorhabditis elegans gene unc-25 encodes glutamic acid decarboxylase and is required for synaptic transmission but not synaptic development."				
RL	J. Neurosci. 19:539-548(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	SPECIES=C.elegans;				
RA	BARLOW K.;				
RL	Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.				
RN	[3]				
RP	SEQUENCE FROM N.A.				

RC SPECIES=C.elegans:  
 RX MEDLINE: 94150718.  
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,  
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HANKINS T., HILLIER L., JIER M., JOHNSTON L.,  
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,  
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARSONS J., PERCY C., RIKKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
 RA SMALLDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,  
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 elegans.";  
 RT Nature 368:32-38(1994).  
 RL EMBL: AF109378; AAD19958.1; -;  
 DR EMBL: AL032626; CAA21537.1; -;  
 SQ SEQUENCE 508 AA; 57792 MW; 3A3EF33 CRC32;

Query Match 73.5%; Score 114; DB 5; Length 508;  
 Best Local Similarity 60.0%; Pred. No. 1.26e-10;  
 Matches 12; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Db 100 PREFNOISGLDPMVAGEN 119  
 1 PRYFNOLSTGLDPMVGLADM 20

RESULT 7  
 ID P70713 PRELIMINARY; PRT; 78 AA.  
 AC P70713;  
 DT 01-FEB-1997 (TEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)  
 DT 01-NOV-1999 (TEMBLrel. 10, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)  
 DE (SULFINOLANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE)  
 DE (FRAGMENT).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER.  
 RA KRAUSKIN I.U., YU X., SMUTZER G., DOTY R.L.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE - HYPOTAURINE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.  
 DR EMBL: U74492; AAB18332.1; -;  
 DR PFAM: PF00282; pyridoxal\_dec. 1.  
 KW Lyase.  
 FT NON\_TER 1 1  
 FT NON\_TER 78 78  
 SQ SEQUENCE 78 AA; 9134 MW; F4808D1F CRC32;

Query Match 51.6%; Score 80; DB 11; Length 78;  
 Best Local Similarity 61.1%; Pred. No. 4.03e-03;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 46 PREFNOISGLDPMVAG 63  
 1 PRYFNOLSTGLDPMVGLAA 18

RESULT 8  
 ID O9Y602 PRELIMINARY; PRT; 267 AA.  
 AC O9Y602;  
 DT 01-NOV-1999 (TEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 1.  
 GN CSAD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA PRITCHARD J.E., RAMSDEN D.B.;  
 RT "Human cysteine sulfonic acid decarboxylase (CSAD)-related mRNA, 1.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF116545; AAD32543.1; -;  
 SQ SEQUENCE 267 AA; 30264 MW; A3475A7D CRC32;

Query Match 51.6%; Score 80; DB 4; Length 267;  
 Best Local Similarity 61.1%; Pred. No. 4.03e-03;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 87 PREFNOISGLDPMVAG 104  
 1 PRYFNOLSTGLDPMVGLAA 18

RESULT 9  
 ID O64577 PRELIMINARY; PRT; 478 AA.  
 AC O64577;  
 DT 01-NOV-1996 (TEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)  
 DE (SULFINOLANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-SPRAGUE-DAWLEY;  
 RA MEDLINE: 95290499.  
 RA KATSUKIA P.J., JERKINS A.A., GOODSPEED D.C., STEELE R.D.;  
 RT "Cloning and characterization of rat cysteine sulfonic acid  
 decarboxylase.";  
 RL Biochim. Biophys. Acta 1262:79-82(1995).  
 CC -1- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE - HYPOTAURINE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 TYRDC).  
 DR EMBL: M64755; AAC42063.1; -;  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; pyridoxal\_dec. 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 478 AA; 53725 MW; 4CAC0093 CRC32;

Query Match 51.6%; Score 80; DB 11; Length 478;  
 Best Local Similarity 61.1%; Pred. No. 4.03e-03;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 87 PREFNOISGLDPMVAG 104  
 1 PRYFNOLSTGLDPMVGLAA 18

RESULT 10  
 ID O9Y600 PRELIMINARY; PRT; 493 AA.  
 AC O9Y600;  
 DT 01-NOV-1999 (TEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 3.  
 GN CSAD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA PRITCHARD J.E., RAMSDEN D.B.;

RT "Human cysteine sulfinic acid decarboxylase (CSAD)-related mRNA, 3.;"  
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF116547; AAD32545.1; -  
 SO SEQUENCE 493 AA; 54951 MW; F4852742 CRC32;

Query Match  
 Best Local Similarity 61.1%; Score 80; DB 4; Length 493;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 87 PREFNOLSTGLDMVGLAA 104  
 11:1111:1111:1111:  
 OY 1 PREFNOLSTGLDMVGLAA 18

RESULT 11  
 ID 064611 PRELIMINARY: PRT: 493 AA.  
 AC 064611:  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, last annotation update)  
 DE CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)  
 DE (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).  
 GN CSD.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 96283809.  
 RA REYMOND I., SERGEANT A., TAPPAZ M.;  
 RT "Molecular cloning and sequence analysis of the cDNA encoding rat  
 RT liver cysteine sulfinate decarboxylase (CSD)."  
 RL Biochim. Biophys. Acta 1307:152-156(1996).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC EMBL: X94152; CAA63868.1; -  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC. 1.  
 DR PFAM: PF00282; Pyridoxal-dec. 1.  
 KW Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 493 AA; 55248 MW; D7A6D9A CRC32;

Query Match  
 Best Local Similarity 61.1%; Score 80; DB 11; Length 493;  
 Matches 11; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 87 PREFNOLSTGLDMVGLAA 104  
 11:1111:1111:1111:  
 OY 1 PREFNOLSTGLDMVGLAA 18

RESULT 12  
 ID 017621 PRELIMINARY: PRT: 387 AA.  
 AC 017621:  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, last sequence update)  
 DT 01-JAN-1999 (TREMblrel. 09, last annotation update)  
 DE C29F7.2 PROTEIN.  
 GN C29F7.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
 OC Rhabditina; Rhabditidae; Peloderinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MCMURRAY A.;  
 RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94150718.  
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LARELLE P.,  
 RA LIGHTNING J., LOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARNSON J., PERCY C., RIFEEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 DR EMBL: 292827; CAB07327.1; -  
 SO SEQUENCE 387 AA; 44178 MW; 7D9B37E1 CRC32;

Query Match  
 Best Local Similarity 47.1%; Score 73; DB 5; Length 387;  
 Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 305 YFDRSLSGLEAKGVKMPW 322  
 11:1111:1111:1111:  
 OY 3 YFDRSLSGLEAKGVKMPW 20

RESULT 13  
 ID 017620 PRELIMINARY: PRT: 394 AA.  
 AC 017620:  
 DT 01-JAN-1998 (TREMblrel. 05, Created)  
 DT 01-JAN-1998 (TREMblrel. 05, last sequence update)  
 DT 01-JAN-1999 (TREMblrel. 09, last annotation update)  
 DE C29F7.1 PROTEIN.  
 GN C29F7.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;  
 OC Rhabditina; Rhabditidae; Peloderinae; Caenorhabditis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MCMURRAY A.;  
 RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94150718.  
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,  
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,  
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,  
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,  
 RA JONES M., KERSHAM J., KIRSTEN J., LAISTER N., LARELLE P.,  
 RA LIGHTNING J., LOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,  
 RA PARNSON J., PERCY C., RIFEEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,  
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,  
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,  
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RT elegans.";  
 RL Nature 368:32-38(1994).  
 DR EMBL: 292827; CAB07326.1; -  
 SO SEQUENCE 394 AA; 44297 MW; 35D9F168 CRC32;

Query Match  
 Best Local Similarity 45.8%; Score 71; DB 5; Length 394;  
 Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Db 311 HYFEKLSAGLEKGVKMPW 329  
 11:1111:1111:1111:  
 OY 2 HYFEKLSAGLEKGVKMPW 20

RESULT 14  
 ID P94758 PRELIMINARY: PRT: 192 AA.  
 AC P94758:  
 DT 01-MAY-1997 (TREMblrel. 03, Created)  
 DT 01-MAY-1997 (TREMblrel. 03, last sequence update)  
 DT 01-NOV-1999 (TREMblrel. 12, last annotation update)  
 DE RIBOKINASE (EC 2.7.1.15).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;



OC Escherichia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12:  
 RX MEDLINE: 97251358.  
 RA ITOH T., AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K.,  
 RA KASAI H., KIMURA S., KITAKAWA M., KITAGAWA M., MAKINO K., MIKI T.,  
 RA MIZOBUCHI K., MORI H., MORI T., MOTOMURA K., NAKADE S., NAKAMURA Y.,  
 RA NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAKPEI G., SEKI Y.,  
 RA SIVASUNDARAM S., TAGAMI H., TAKEDA J., TAKEMOTO K., WADA C.,  
 RA YAMAMOTO Y., HORIUCHI T.;  
 RT "A 450-kb DNA sequence of the Escherichia coli K-12 genome  
 RT corresponding to the 40,1-50.0 min region on the linkage map";  
 RL DNA Res. 3:379-392(1996).  
 DR EMBL: D90848; BAA15968.1;  
 DR PFAM: PF00294; pfkb; 1.  
 KW Kinase.  
 SO SEQUENCE 192 AA; 20544 MW; 1A02381C CRC32;

Query Match 43.9%; Score 68; DB 2; Length 192;  
 Best Local Similarity 45.0%; Pred. No. 8.70e-01;  
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Db 16 PALFFRLSTGLARELLVEM 35  
 QY 1 PRYFQQLSTGLDMVGLADW 20

RESULT 15  
 ID 052961 PRELIMINARY: PRT: 169 AA.  
 AC 052961.  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)  
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
 DE ORF14.  
 OS Sinorhizobium meliloti.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-RU11001;  
 RX MEDLINE: 97474264.  
 RA PLATZER J., STERR W., HAUSMANN M., SCHMITT R.;  
 RT "Three genes of a motility operon and their role in flagellar rotary  
 RT speed variation in Rhizobium meliloti."  
 RL J. Bacteriol. 179:6391-6399(1997).  
 DR EMBL: L49337; AAB81407.1;  
 SO SEQUENCE 169 AA; 18440 MW; D1356C2A CRC32;

Query Match 43.2%; Score 67; DB 2; Length 169;  
 Best Local Similarity 72.7%; Pred. No. 1.33e+00;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 24 PRYFPDLDTGL 34  
 QY 1 PRYFQQLSTGL 11

Search completed: Tue Mar 7 21:43:28 2000  
 Job time : 13 secs.

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##residues 1-585 #label ERL  
##cross-references GB:M72422; NID:g204225; PIDN:AAA63488.1; PID:g204226  
#experimental\_source brain  
#note the authors translated the codon GAT for residue 86 as His, TCA for residue 198 as Ala, and CAG for residue 428 as Trp

REFERENCE A60888  
#authors Chang, Y.C.; Gottlieb, D.I.  
#journal J. Neurosci. (1988) 8:2123-2130  
#title Characterization of the proteins purified with monoclonal antibodies to glutamic acid decarboxylase.  
#cross-references MUID:88258610  
#accession A60888  
##status preliminary  
##molecule\_type protein  
##residues 'V', 191-194, 'X', 196-203, 'XX', 206-219, 'X', 225-234, 'X', 236-247, 'X', 249-266, 'X', 524-537, 539-543, 'V', 547-549, 'X', 551-553, 'X', 555-558 #label CHA  
#comment This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 396  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted

SUMMARY #length 585 #molecular-weight 65402 #checksum 7756

Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 1,21e-17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFLLEYVTLKKMR 225  
|||||  
1 TYEIAPVFLLEYVTLKKMR 20

RESULT 3  
ENTRY A41292 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 13-May-1992 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS A41935; A41292; S30058; B54778  
REFERENCE A41935  
#authors Bu, D.F.; Erlanger, M.G.; Hiltz, B.C.; Tiliakaratne, N.J.K.; Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J.

#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.  
#cross-references MUID:92196068  
#accession A41935  
##molecule\_type mRNA  
##residues 1-585 #label BU1  
##cross-references GB:M81882; NID:g182933; PIDN:AAA62367.1; PID:g182934  
#experimental\_source brain  
#note #sequence extracted from NCBI backbone (NCBI:88007)

REFERENCE A41292  
#authors Karlsson, A.E.; Hagopian, W.A.; Grubin, C.E.; Dube, S.; Distelche, C.M.; Adler, D.A.; Baermeier, H.; Mathewes, S.; Grant, F.J.; Foster, D.; Lemark, A.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8337-8341  
#title Cloning and primary structure of a human islet isoform of glutamic acid decarboxylase from chromosome 10.  
#cross-references MUID:92020648  
#accession A41292  
##molecule\_type mRNA  
##residues 1-585 #label KAR  
##cross-references GB:M74826; NID:g182931; PIDN:AAA56491.1; PID:g182932  
#experimental\_source pancreatic islet

REFERENCE S30058  
#authors Mauch, L.; Ahney, C.C.; Berg, H.; Scherbaum, W.A.; Liedvogel, B.; Northmann, W.  
#journal Eur. J. Biochem. (1993) 212:597-603  
#title Characterization of a linear epitope within the human pancreatic 64-kDa glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients.

#cross-references MUID:93185681  
#accession S30058  
##molecule\_type mRNA  
##residues 6-585 #label MAU  
#cross-references EMBL:X69936  
#experimental\_source pancreatic islet

REFERENCE A54778  
#authors Bu, D.F.; Tobin, A.J.  
#journal Genomics (1994) 21:222-228  
#title The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral GAD.

#cross-references MUID:94375018  
#contents annotation; Intron-exon boundaries

COMMENT This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene. GAD has also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.

GENETICS GDB:GAD2  
#gene  
##cross-references GDB:128595; OMIM:138275  
#map\_position 10p11.23-10p11.23  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 396  
#binding-site pyridoxal phosphate (Lys) (covalent)  
#status predicted

SUMMARY #length 585 #molecular-weight 65411 #checksum 4799

Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 1,21e-17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFLLEYVTLKKMR 225  
|||||  
1 TYEIAPVFLLEYVTLKKMR 20

RESULT 4  
ENTRY S38533 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 2 - mouse  
ALTERNATE\_NAMES glutamate decarboxylase GAD65; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Mus musculus #common\_name house mouse  
DATE 20-May-1994 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS S38533  
REFERENCE S38533  
#authors Lee, D.S.; Tian, J.; Phan, T.; Kaufman, D.L.  
#journal Biochim. Biophys. Acta (1993) 1216:157-160  
#title Cloning and sequence analysis of a murine cDNA encoding glutamate decarboxylase (GAD65).  
#cross-references MUID:94032481  
#accession S38533  
##status preliminary  
##molecule\_type mRNA  
##residues 1-585 #label LEE  
##cross-references GB:L10980; NID:g413867; PIDN:AAA93049.1; PID:g413868  
#comment This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal

```
FEATURE phosphate
396 #binding-site pyridoxal phosphate (Lys) (covalent)
#status predicted
SUMMARY #length 585 #molecular-weight 65224 #checksum 7599

Query Match 100.0%; Score 155; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.21e-17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAVFVLEVTLKMR 225
QY 1 TYEIAVFVLEVTLKMR 20

RESULT 5
ENTRY JC4064 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 65K chain - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
22-Jun-1999
ACCESSIONS JC4064
REFERENCE JC4064
#authors Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
#journal Gene (1995) 152:257-260
#title Sequences of two porcine glutamic acid decarboxylases (65-and
67-kDa GAD).
#cross-references MUID:95137399
#accession JC4064
#molecule_type mRNA
#residues 1-585 #label SUZ
#cross-references DDBJ:D31848; NID:g790964; PIDN:BA0635.1;
PID:d1007207; PID:g790965

COMMENT ##experimental_source brain
This enzyme catalyzes the conversion of glutamic acid into
gamma-amino butyric acid.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
FEATURE 393-396 #domain DOPA decarboxylase binding #status predicted
#label BIN
SUMMARY #length 585 #molecular-weight 65388 #checksum 5933
Query Match 100.0%; Score 155; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.21e-17;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAVFVLEVTLKMR 225
QY 1 TYEIAVFVLEVTLKMR 20

RESULT 6
ENTRY 153274 #type fragment
TITLE glutamate decarboxylase, 67K, brain - mouse (fragment)
ORGANISM #formal_name Mus sp. #common_name mouse
DATE 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change
16-Feb-1997
ACCESSIONS 153274
REFERENCE 153274
#authors Faulkner-Jones, B.E.; Gram, D.S.; Kun, J.; Harrison, L.C.
#journal Endocrinology (1993) 133:2962-2972
#title Localization and quantitation of expression of two glutamate
decarboxylase genes in pancreatic beta-cells and other
peripheral tissues of mouse and rat.
#cross-references MUID:94062679
#accession 153274
#status preliminary: translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-206 #label RES
#cross-references GB:S67453; NID:g456853
CLASSIFICATION #superfamily human glutamate decarboxylase
SUMMARY #length 206 #checksum 3323

FEATURE phosphate
396 #binding-site pyridoxal phosphate (Lys) (covalent)
#status predicted
SUMMARY #length 585 #molecular-weight 65224 #checksum 7599

Query Match 84.5%; Score 131; DB 2; Length 206;
Best Local Similarity 85.0%; Pred. No. 2.07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 17 TYEIAVFVLEVTLKMR 36
QY 1 TYEIAVFVLEVTLKMR 20

RESULT 7
ENTRY S61534 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 62K isoform - mouse
ALTERNATE_NAMES glutamic acid decarboxylase
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change
22-Jun-1999
ACCESSIONS S61534; S61533
REFERENCE S61534
#authors Katarova, Z.; Szabo, G.; Mugnaini, E.; Greenspan, R.J.
#journal Eur. J. Neurosci. (1990) 2:190-202
#title Molecular identification of the 62 kd form of glutamic acid
decarboxylase from the mouse.
#accession S61534
#molecule_type mRNA
#residues 1-585 #label KAT
#cross-references EMBL:24976
#experimental_source brain
REFERENCE S61533
#authors Szabo, G.
#submission submitted to the EMBL Data Library, June 1995
#accession S61533
#molecule_type mRNA
#residues 1-554, 'YQPGDKANFRRWYSNPASQSDIDFLTEIERLGDL' #label
52A

#cross-references EMBL:24976; NID:g886686; PIDN:CAA90277.1;
PID:g886687
#experimental_source brain
#note the differences at the carboxyl end are due to a
frameshift error

CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS carbon-carbon lyase; carboxy-lyase
SUMMARY #length 585 #molecular-weight 65381 #checksum 5716
Query Match 84.5%; Score 131; DB 2; Length 585;
Best Local Similarity 85.0%; Pred. No. 2.07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAVFVLEVTLKMR 233
QY 1 TYEIAVFVLEVTLKMR 20

RESULT 8
ENTRY A41367 #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - rat
ALTERNATE_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 12-Jun-1992 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
ACCESSIONS A41367; A43756; JH0195
REFERENCE A41367
#authors Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.;
Dyrberg, T.; Madsen, O.D.
#journal Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758
#title Cloning, characterization, and autoimmune recognition of rat
islet glutamic acid decarboxylase in insulin-dependent
diabetes mellitus.
#cross-references MUID:92020930
#accession A41367
#status preliminary
#molecule_type mRNA
#residues 1-593 #label MIC
```

##cross-references GB:M76177; NID:g204227; PIDN:AAA41184.1; PID:g204228  
REFERENCE A43756  
#authors Wyborski, R.J.; Bond, R.W.; Gottlieb, D.I.  
#journal Brain Res. Mol. Brain Res. (1990) 8:193-198  
#title Characterization of a cDNA coding for rat glutamic acid decarboxylase.  
#cross-references MUID:91014554  
#accession A43756  
#status preliminary  
#molecule-type mRNA  
#residues 1-593 #label WTB  
#cross-references GB:X57573; NID:g56183; PIDN:CAA40801.1; PID:g56184  
#note the authors translated the codon TGT for residue 412 as Ser and TCT for residue 413 as Cys

REFERENCE JH0195  
#authors Julien, J.F.; Samama, P.; Mallet, J.  
#journal J. Neurochem. (1990) 54:703-705  
#title Rat brain glutamic acid decarboxylase sequence deduced from a cloned cDNA.  
#cross-references MUID:90132703  
#accession JH0195  
#molecule-type mRNA  
#residues 1-102, 'V', 104-283, 'S', 285-286, 'AD', 289-343, 'EA', 346, 'I', 348-351, 'LE', 354-379, 'R', 381-593 #label JUL  
#cross-references GB:X57572; NID:g56185; PIDN:CAA40800.1; PID:g56186  
#comment This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene.

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal phosphate

FEATURE 404  
#binding-site pyridoxal phosphate (lys) (covalent)  
#status predicted

SUMMARY #length 593 #molecular-weight 66640 #checksum 3971

Query Match 84.5%; Score 131; DB 1; Length 593;  
Best Local Similarity 85.0%; Pred. No. 2.07e-12;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAPVFLVLEVTILKKMR 233  
|||||||:|:|||||  
Oy 1 TYEIAPVFLVLEVTILKKMR 20

RESULT 9  
ENTRY S48135 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 14-Jul-1995 #sequence\_revision 10-Nov-1995 #text\_change 07-May-1999

ACCESSIONS S48135  
REFERENCE S48135  
#authors Kelly, C.D.; Edwards, Y.; Johnstone, A.P.; Harfst, E.; Nogradi, A.; Nussey, S.S.; Povey, S.; Carter, N.D.; Ann. Hum. Genet. (1992) 56:255-265  
#note Nucleotide sequence and chromosomal assignment of a cDNA encoding the large isoform of human glutamate decarboxylase.  
#cross-references MUID:93080286  
#accession S48135  
#molecule-type mRNA  
#residues 1-593 #label KEL  
#journal #cross-references EMBL:222750  
CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66952 #checksum 4836

Query Match 84.5%; Score 131; DB 2; Length 593;  
Best Local Similarity 85.0%; Pred. No. 2.07e-12;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAPVFLVLEVTILKKMR 233

Oy 1 TYEIAPVFLVLEVTILKKMR 20  
|||||||:|:|||||

RESULT 10  
ENTRY S51776 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) - human  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 15-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Feb-1997

ACCESSIONS S51776  
REFERENCE S51775  
#authors Johnstone, A.  
#submission submitted to the EMBL Data Library, May 1993  
#accession S51776  
#status preliminary  
#molecule-type mRNA  
#residues 1-593 #label JOH  
#cross-references EMBL:222750  
#note this is an unpublished revision to the sequence from reference S48135

CLASSIFICATION #superfamily human glutamate decarboxylase  
KEYWORDS carbon-carbon lyase; carboxy-lyase  
SUMMARY #length 593 #molecular-weight 66946 #checksum 4842

Query Match 84.5%; Score 131; DB 2; Length 593;  
Best Local Similarity 85.0%; Pred. No. 2.07e-12;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAPVFLVLEVTILKKMR 233  
|||||||:|:|||||  
Oy 1 TYEIAPVFLVLEVTILKKMR 20

RESULT 11  
ENTRY B41935 #type complete  
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - human  
ALTERNATE\_NAMES glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase  
ORGANISM #formal\_name Homo sapiens #common\_name man  
DATE 31-Dec-1993 #sequence\_revision 23-Mar-1995 #text\_change 18-Jun-1999

ACCESSIONS B41935; JH0805; A61406; PQ0157; PQ0158; B41367; A36463; A54778

REFERENCE A41935  
#authors Bu, D.F.; Erlander, M.G.; Hitz, B.C.; Tiliakaratne, N.J.K.; Kaufman, D.L.; Wagner-McPherson, C.B.; Evans, G.A.; Tobin, A.J.  
#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:2115-2119  
#title Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.  
#cross-references MUID:92196068  
#accession B41935  
#molecule-type mRNA  
#residues 1-594 #label BUI  
#cross-references GB:M81883; NID:g182935; PIDN:AAA62368.1; PID:g182936  
#experimental\_source pancreatic islet  
#note sequence extracted from NCBI backbone (NCBIP:88006)

REFERENCE JH0805  
#authors Kawasaki, E.; Moriyuchi, R.; Watanabe, M.; Satoh, K.; Charles Brunicardi, F.; Malt, P.C.; Yamaguchi, T.; Nagataki, S.; Akazawa, S.; Miyamoto, T.; Nagataki, S.  
#journal Biochem. Biophys. Res. Commun. (1993) 192:1353-1359  
#title Cloning and expression of large isoform of glutamic acid decarboxylase from human pancreatic islet.  
#cross-references MUID:93282845  
#accession JH0805  
#molecule-type mRNA  
#residues 1-117, 'N', 119-30, 'N', 32-67, 'K', 69-115, 'L', 117-154, 'T', 156-301, 'C', 303-476, 'G', 478-491, 'G', 493-594 #label KAW  
#cross-references GB:S61898; NID:g385310; PIDN:AA82698.1; PID:g385311  
#experimental\_source pancreatic islet  
REFERENCE JH0806

**#authors** Yamashita, K.; Cram, D.S.; Harrison, L.C.  
**#journal** Biochem. Biophys. Res. Commun. (1993) 192:1347-1352  
**#title** Molecular cloning of full-length glutamic acid decarboxylase 67 from human pancreas and islets.  
**#cross-references** MUID:93282844  
**#accession** JH0806  
**#molecule\_type** mRNA  
**#residues** 1-67, 'K', 69-435, 'L', 437-511, 'S', 513-594 ##label YAM  
**#cross-references** GB:S61897; NID:g9355450; PIDW:AA82937.1; PID:g935451  
**#experimental\_source** pancreatic islet  
**REFERENCE**  
**#authors** Kelly, C.; Carter, N.D.; Johnstone, A.P.; Nussey, S.S.  
**#journal** Lancet (1991) 338:1468-1469  
**#title** Cloning of large isoform of human brain glutamic acid decarboxylase.  
**#cross-references** MUID:92065769  
**#accession** A61406  
**#molecule\_type** mRNA  
**#residues** 62-67, 'K', 69-205, 'N', 207-564, 'L', 566-594 ##label KEL  
**#experimental\_source** brain  
**REFERENCE**  
**#authors** Cram, D.S.; Barnett, L.D.; Joseph, J.L.; Harrison, L.C.  
**#journal** Biochem. Biophys. Res. Commun. (1991) 176:1239-1244  
**#title** Cloning and partial nucleotide sequence of human glutamic acid decarboxylase cDNA from brain and pancreatic islets.  
**#cross-references** MUID:91248209  
**#accession** P00157  
**#molecule\_type** mRNA  
**#residues** 218-463 ##label CRL  
**#cross-references** GB:M70434  
**#experimental\_source** brain  
**#accession** P00158  
**#molecule\_type** mRNA  
**#residues** 218-234, 'K', 236-240, 'N', 242-288, 'H', 290-323, 'L', 325-329  
**#cross-references** GB:M70435; NID:g182941; PIDW:AA55513.1; PID:g182942  
**#experimental\_source** pancreatic islet  
**REFERENCE**  
**#authors** Michelsen, B.K.; Petersen, J.S.; Boel, E.; Moldrup, A.; Dyrberg, T.; Madsen, O.D.  
**#journal** Proc. Natl. Acad. Sci. U.S.A. (1991) 88:8754-8758  
**#title** Cloning, characterization, and autoimmune recognition of rat islet glutamic acid decarboxylase in insulin-dependent diabetes mellitus.  
**#cross-references** MUID:92020930  
**#accession** B41367  
**#molecule\_type** mRNA  
**#residues** 317-482, 'R', 484-594 ##label MIT  
**REFERENCE**  
**#authors** Persson, H.; Peltö-Huikko, M.; Metsis, M.; Seoder, O.; Brenne S.; Skog, S.; Hoekfelt, T.; Ritzen, E.M.  
**#journal** Mol. Cell. Biol. (1990) 10:4701-4711  
**#title** Expression of the neurotransmitter-synthesizing enzyme glutamic acid decarboxylase in male germ cells.  
**#cross-references** MUID:90355966  
**#accession** A36463  
**#molecule\_type** mRNA  
**#residues** 527-594 ##label PER  
**#cross-references** GB:M5574; NID:g182929; PIDW:AA72938.1; PID:g182930  
**REFERENCE**  
**#authors** Bu, D.F.; Tobin, A.J.  
**#journal** Genomics (1994) 21:222-228  
**#title** The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD-67 and GAD-65) suggests that they derive from a common ancestral GAD.  
**#cross-references** MUID:94375018  
**#contents** annotation: intron-exon organization  
**COMMENT** This enzyme (GAD) catalyzes the formation of an inhibitory neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid; it has several isoforms, each encoded by a separate gene. GAD has also been implicated as an autoantigen in autoimmune disease stiff-man syndrome and insulin-dependent diabetes mellitus.

```

GENETICS
#gene GDB:GAD1: GAD
##cross-references GDB:119244: OMIM:266100
CLASSIFICATION
#map_position 2q31-2q31
#superfamily human glutamate decarboxylase
KEYWORDS
alternative splicing; carbon-carbon lyase; carboxy-lyase;
phosphoprotein; pyridoxal phosphate
FEATURE
405 #binding_site pyridoxal phosphate (Lys) (covalent)
#status predicted
SUMMARY
#length 594 #molecular_weight 66924 #checksum 6189
Query Match 84.5%; Score 131; DB 1; Length 594;
Best Local Similarity 85.0%; Pred. No. 2, 07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 215 TTYIAPVFLVLEMDITLKKMR 234
|||||:|:|:|:|
QY 1 TTYIAPVFLVLEVTLLKKMR 20

RESULT 12
ENTRY #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change
22-Jun-1999
ACCESSIONS
S51775
REFERENCE
S51775
#authors Johnstone, A.
#submission submitted to the EMBL Data Library, May 1993
#accession S51775
#status preliminary
##molecule_type mRNA
##residues 1-594 ##label JOH
##cross-references EMBL:22750; NID:g298098; PIDW:CAA80435.1;
PID:g298099
CLASSIFICATION
#superfamily human glutamate decarboxylase
KEYWORDS
carbon-carbon lyase; carboxy-lyase
SUMMARY
#length 594 #molecular_weight 66973 #checksum 6437
Query Match 84.5%; Score 131; DB 2; Length 594;
Best Local Similarity 85.0%; Pred. No. 2, 07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 215 TTYIAPVFLVLEMDITLKKMR 234
|||||:|:|:|:|
QY 1 TTYIAPVFLVLEVTLLKKMR 20

RESULT 13
ENTRY #type complete
TITLE glutamate decarboxylase (EC 4.1.1.15) 1 - cat
ALTERNATE_NAMES
glutamate decarboxylase GAD67; L-glutamate 1-carboxy-lyase
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE 31-Dec-1993 #sequence_revision 23-Mar-1995 #text_change
18-Jun-1999
ACCESSIONS
A46758; A45671
REFERENCE
A46758
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#submission submitted to GenBank, September 1989
#accession A46758
##molecule_type mRNA
##residues 1-594 ##label KOB
##cross-references CB:M8629; NID:g163858; PIDN:AAA51450.1; PID:g163859
A45671
REFERENCE
A45671
#authors Kobayashi, Y.; Kaufman, D.L.; Tobin, A.J.
#journal J. Neurosci. (1987) 7:2768-2772
#title Glutamic acid decarboxylase cDNA: nucleotide sequence
encoding an enzymatically active fusion protein.
#cross-references MIMD:87310623
#accession A45671
##molecule_type mRNA

```

```
#residues      1-558,'RGPRPFGSGSSRRQILHSPIITSSSR' ##label K02
#note          This sequence has been revised in reference A6758
COMMENT        This enzyme (GAD) catalyzes the formation of an inhibitory
                neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
                it has several isoforms, each encoded by a separate gene.

GENETICS
#gene          GADI
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS       carbon-carbon lyase; carboxy-lyase; phosphoprotein; pyridoxal
               phosphate
FEATURE
F005           #binding_site pyridoxal phosphate (lys) (covalent)
SUMMARY        #status predicted
               #length 594 #molecular-weight 66824 #checksum 5630

Query Match    84.5%; Score 131; DB 1; Length 594;
Best Local Similarity 85.0%; Pred. No. 2,07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db   215 TYEIAPVFLMEQTLLKKM 234
     |||||:::||||:|||||
OY   1 TYEIAPVFLLEVTLTKMR 20

RESULT 14
ENTRY   JC4065             #type complete
TITLE   glutamate decarboxylase [EC 4.1.1.15] 6Tk chain - pig
ORGANISM #formal_name Sus scrofa domestica #common_name domestic pig
DATE     30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change
         22-Jun-1999

ACCESSIONS
REFERENCE   JC4064
            Suzuki, R.; Asami, N.; Amann, E.; Wagatsuma, M.
            Gene (1995) 152:257-260
            Sequences of two porcine glutamic acid decarboxylases (65-and
            67-kDa GAD).
#cross-references MFID:95137399
#accesion      JC4065
              #molecule_type mRNA
              #residues      1-594 ##label SUZ
              #cross-references DDBJ:D31849; NID:g790966; PIDN:BAA06636.1;
                  PIR:d1007208; PIR:g790967

COMMENT      ##experimental_source brain
              This enzyme catalyzes the conversion of glutamic acid into
              gamma-amino butyric acid.
CLASSIFICATION #superfamily human glutamate decarboxylase
KEYWORDS      carbon-carbon lyase; carboxy-lyase
FEATURE
F002-405     #domain DOPA decarboxylase binding #status predicted
              #label BIN
SUMMARY      #length 594 #molecular-weight 66894 #checksum 5491

Query Match    84.5%; Score 131; DB 2; Length 594;
Best Local Similarity 85.0%; Pred. No. 2,07e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db   215 TYEIAPVFLMEQTLLKKM 234
     |||||:::::||:|||||
OY   1 TYEIAPVFLLEVTLTKMR 20

RESULT 15
ENTRY   A30999             #type complete
TITLE   glutamate decarboxylase (Ec 4.1.1.15) C1 - fruit fly
ALTERNATE_NAMES Drosophila melanogaster )
ORGANISM      L-glutamate 1-carboxy-lyase
DATE          #formal_name Drosophila melanogaster
              26-Oct-1989 #sequence_revision 23-Mar-1995 #text_change
              18-Jun-1999
ACCESSIONS   JH0192; PS0301; A30999
REFERENCE     JH0192
              Jackson, F.R.; Newby, L.M.; Kulikarni, S.J.
              J. Neurochem. (1990) 54:1068-1078
```

```

#title      Drosophila GABAergic systems: sequence and expression of
            glutamic acid decarboxylase.
#cross-references  MIMD:90155291
#accession  JH0192
#molecule-type  mRNA
#residues   1-510 ##label  JAC
#cross-references  GR:X76198; NID:g433082; PIDN:CMA53791.1; PID:g433083
#accession  PS0301
##molecule-type  mRNA
#residues    156-200, 'F', 202-300, 'K', 302-384, 'L', 386-510 ##label  JA2
COMMENT      This enzyme (GAD) catalyzes the formation of an inhibitory
            neurotransmitter, gamma-aminobutyric acid, from L-glutamic acid;
            it has several isoforms, each encoded by a separate gene.

GENERIC5
#gene        FlyBase:Gadi
            ##cross-references  FlyBase:FBgn00004516
CLASSIFICATION  #superfamily human glutamate decarboxylase
KEYWORDS       carbon-lyase; carboxy-lyase; phosphoprotein; pyridoxal
            phosphate
FEATURE
322           #binding_site pyridoxal phosphate (Lys) (covalent)
            #status predicted
SUMMARY        #length 510 #molecular-weight 57758 #checksum 3194

Query Match      79.4%; Score 123; DB 1; Length 510;
Best Local Similarity 75.0%; Pired. No. 1, 02e-10;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db      132  TYELAPVFIIMENVLTKRM 151
        |||||:::|::| 1 1 |||
0y      1  TYELAPVFIILEVYTLTKRM 20

```

Search completed: Tue Mar 7 21:52:32 2000  
Job time : 8 secs.



\*\*\*\*\*  
MUSE  
\*\*\*\*\*  
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Msrch\_bp protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Mar 7 21:50:04 2000. Maspar time 3.46 Seconds  
Tabular output not generated. 172.707 Million cell updates/sec

Title: >US-08-981-824-6  
Description: (1-20) from US08981824.pep  
Perfect Score: 155  
Sequence: 1 TYLEIAPFVLEVTLLKMR 20

Scoring table: PAM 150  
Gap 15

Searched: 82229 seqs 29864866 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot38  
1:swissprot

Statistics: Mean 31.080; Variance 42.635; scale 0.729

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	155	100.0	585	1 DCE2_RAT	GLUTAMATE DECARBOXYLASE	6.44e-21
2	155	100.0	585	1 DCE2_PIG	GLUTAMATE DECARBOXYLASE	6.44e-21
3	155	100.0	585	1 DCE2_HUMAN	GLUTAMATE DECARBOXYLASE	6.44e-21
4	155	100.0	585	1 DCE2_MOUSE	GLUTAMATE DECARBOXYLASE	6.44e-21
5	131	84.5	593	1 DCE1_MOUSE	GLUTAMATE DECARBOXYLASE	6.98e-15
6	131	84.5	593	1 DCE1_RAT	GLUTAMATE DECARBOXYLASE	6.98e-15
7	131	84.5	594	1 DCE1_PIG	GLUTAMATE DECARBOXYLASE	6.98e-15
8	131	84.5	594	1 DCE1_HUMAN	GLUTAMATE DECARBOXYLASE	6.98e-15
9	131	84.5	594	1 DCE1_FEICA	GLUTAMATE DECARBOXYLASE	6.98e-15
10	123	79.4	510	1 DCE1_DROME	GLUTAMATE DECARBOXYLASE	6.19e-13
11	74	47.7	298	1 YC34_HELPY	HYPOTHETICAL PROTEIN H	4.19e-02
12	70	45.2	353	1 GBI_HELI	GUANINE NUCLEOTIDE-BIN	2.41e-01
13	70	45.2	353	1 RECG_LYMT	ATP-DEPENDENT DNA HELI	5.63e-01
14	68	43.9	682	1 RECG_BACSU	SUCCINATE DEHYDROGENS	8.56e-01
15	67	43.2	202	1 DHC_BACSU	HYPOTHETICAL 46.2 KD P	8.56e-01
16	67	43.2	406	1 YC9_EUGGR	HYPOTHETICAL 52.1 KD P	1.95e+00
17	65	41.9	477	1 YG1_ECOLI	PHOSPHO-N-ACETYLMURAO	2.93e+00
18	64	41.3	324	1 MRAY_BACSU	ACTIVATOR 140 KD SUB	2.93e+00
19	64	41.3	1147	1 AC15_HUMAN	GENOME POLYPROTEIN [CO	4.36e+00
20	64	41.3	3412	1 POLG_TBVEV	SHORT CHAIN 3-HYDROXYA	4.36e+00
21	63	40.6	307	1 HCDH_PIG	SHORT CHAIN 3-HYDROXYA	4.36e+00
22	63	40.6	314	1 HCDH_HUMAN	SHORT CHAIN 3-HYDROXYA	4.36e+00
23	63	40.6	314	1 HCDH_MOUSE	SHORT CHAIN 3-HYDROXYA	4.36e+00

ID	DESCRIPTION	SCORE	ALIGNMENT
24	GBI_ASTPE	40.6	353 1
25	STD_METH	40.6	437 1
26	RRO_CNV	40.6	817 1
27	SEG8_BPT4	40.0	229 1
28	YGI1_YEAST	40.0	278 1
29	YGI1_YEAST	40.0	355 1
30	YGI1_YEAST	40.0	430 1
31	YGI1_YEAST	40.0	459 1
32	YGI1_YEAST	40.0	3414 1
33	YGI1_YEAST	40.0	3414 1
34	YGI1_YEAST	40.0	200 1
35	YGI1_YEAST	40.0	312 1
36	YGI1_YEAST	40.0	391 1
37	YGI1_YEAST	40.0	761 1
38	YGI1_YEAST	40.0	293 1
39	YGI1_YEAST	40.0	355 1
40	YGI1_YEAST	40.0	449 1
41	YGI1_YEAST	40.0	449 1
42	YGI1_YEAST	40.0	1131 1
43	YGI1_YEAST	40.0	1394 1
44	YGI1_YEAST	40.0	266 1
45	YGI1_YEAST	40.0	301 1

## ALIGNMENTS

RESULT 1  
ID DCE2\_RAT STANDARD: PRT: 585 AA.  
AC 005683:  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
GN GAD2 OR GAD65.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Eukaryota; Rodentia; Sciurognathi; Muridae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HIPPOCAMPUS;  
RX MEDLINE: 91289343;  
RA ERLANDER M.G., TILAKARATNE N.J., FELDBLUM S., PATEL N.,  
RT TOBIN A.J.;  
RL "Two genes encode distinct glutamate decarboxylases.";  
RL Neuron 7:91-100(1991).  
CC -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
CC -!- CATALYTIC ACTIVITY: L-GLUTAMATE -> 4-AMINOBUTANOATE + CO(2).  
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -!- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
CC DECARBOXYLASE.  
CC  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL: M72422; AAA63488.1;  
DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC. 1.  
DR PIRAM: PF00282; pyridoxal\_dec. 1.  
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
KW Pyridoxal phosphate; Multigene family;  
FT BINDING 396 396 PYRIDOXAL PHOSPHATE (POTENTIAL).  
SQ SEQUENCE 585 AA; 65402 MW; E35D601A CRC32;

Query Match 100.0%; Score 155; DB 1; Length 585;  
Best Local Similarity 100.0%; Pred. No. 6.44e-21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFVLEVTYTLKMR 225  
 ||||||||||||||||  
 QY 1 TYEIAPVFVLEVTYTLKMR 20

RESULT 2  
 ID DCE2.PIG STANDARD: PRT: 585 AA.

AC P48321;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 GN (65 KD GLUTAMIC ACID DECARBOXYLASE).

OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 95137399.

RA SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;  
 "Sequences of two porcine glutamic acid decarboxylases (65- and 67-kDa GAD).";

RT Gene 152:257-260(1995).  
 RL -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.

CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYROC).

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CC EMBL: D31848; BAA0635.1;  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; pyridoxal.dec.1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 396 PYRIDOXAL PHOSPHATE (POTENTIAL).  
 SQ SEQUENCE 585 AA; 65388 MW; F3E9BD88 CRC32.

Query Match 100.0%; Score 155; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 6,44e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFVLEVTYTLKMR 225  
 ||||||||||||||||  
 QY 1 TYEIAPVFVLEVTYTLKMR 20

RESULT 3  
 ID DCE2.HUMAN STANDARD: PRT: 585 AA.

AC 005329;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 GN (65 KD GLUTAMIC ACID DECARBOXYLASE).

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo..  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92196068.  
 BU D.-F., ERLANDER M.G., HITZ B.C., TILLAKARATNE N.J., KAUFMAN D.L.,

RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;  
 "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are each encoded by a single gene.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).  
 RL [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE: 94375018.  
 RA BU D.-F., TOBIN A.J.;  
 "The exon-intron organization of the genes (GAD1 and GAD2) encoding two human glutamate decarboxylases (GAD67 and GAD65) suggests that they derive from a common ancestral GAD.";  
 RL Genomics 21:222-228(1994).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC TISSUE-PANCREATIC ISLETS;  
 RX MEDLINE: 92020848.  
 RA KARLSEN A.E., HAGOPIN W.A., GRUBIN C.E., DUBE S., DISTECHE C.M.,  
 RA ADLER D.A., BARMEIER H., MATHIENS S., GRANT F.J., FOSTER D.,  
 RA LERNMARK A.;

RT "Cloning and primary structure of a human islet isoform of glutamic acid decarboxylase from chromosome 10.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:8337-8341(1991).  
 RN [4]

RP SEQUENCE OF 6-585 FROM N.A.  
 RC TISSUE-PANCREAS;  
 RX MEDLINE: 93185681.

RA MAUCH L., ABNEY C.C., BERG H., SCHERBAUM W.A., LIEBVOGEL B.,  
 RA NORTHEMANN W.;

RT "Characterization of a linear epitope within the human pancreatic 64-kDa glutamic acid decarboxylase and its autoimmune recognition by sera from insulin-dependent diabetes mellitus patients.";  
 RT Eur. J. Biochem. 212:597-603(1993).

RL -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.

CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE DECARBOXYLASE.

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CC EMBL: M81882; AAA62367.1;  
 DR EMBL: M74826; AAA58491.1;  
 DR EMBL: X69936; CAA49554.1; ALT\_INIT.  
 DR EMBL: M70435; AAA52513.1;  
 DR PIR: A41292; A41292.  
 DR PIR: P00158; P00158.  
 DR MIM: 138275;

DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; pyridoxal.dec.1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family.  
 FT BINDING 396 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 585 AA; 65411 MW; 8AD62B62 CRC32;

Query Match 100.0%; Score 155; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 6,44e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFVLEVTYTLKMR 225  
 ||||||||||||||||  
 QY 1 TYEIAPVFVLEVTYTLKMR 20

RESULT 4  
 ID DCE2.MOUSE STANDARD: PRT: 585 AA.  
 AC P48320; O35519;

DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65)  
 DE (65 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD2 OR GAD65.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=BRAIN;  
 RX MEDLINE: 94032481.  
 RA LEE D.S., TIAN J., PHAN T., KAUFMAN D.L.;  
 RT "Cloning and sequence analysis of a murine cDNA encoding glutamate  
 RT decarboxylase (GAD65)."  
 RL Biochim. Biophys. Acta 1216:157-160(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6; TISSUE=BRAIN;  
 RX MEDLINE: 97115675.  
 RA ASADA H., KAWAMURA Y., MARIYAMA K., KUME H., DING R.G., JI F.Y.,  
 RA KAWABARA N., KUZUME H., SANBO M., YAGI T., OBATA K.;  
 RT "Mice lacking the 65 kDa isoform of glutamic acid decarboxylase  
 RT (GAD65) maintain normal levels of GAD67 and GABA in their brains but  
 RT are susceptible to seizures."  
 RL Biochem. Biophys. Res. Commun. 229:891-895(1996).  
 RN [3]  
 RP SEQUENCE OF 175-379 FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localization and quantitation of expression of two glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat."  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: LOCAL TO DOPA DECARBOXYLASE, AND TO PLP-TYPE HISTIDINE  
 CC DECARBOXYLASE.  
 CC -----  
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 CC -----  
 DR EMBL: L16980; AAA93049.1; -;  
 DR EMBL: DA2051; BAA22893.1; -;  
 DR EMBL: S67454; CAB32806.1; -;  
 DR MGD: MGI:95634; GAD2.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFM: PFM00282; pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family;  
 FT BINDING 396  
 FT CONFLICT 259  
 FT CONFLICT 319  
 FT CONFLICT 325  
 FT CONFLICT 499  
 SO SEQUENCE 585 AA; 65224 MM; 985C088 CRC32;

Query Match 100.0%; Score 155; DB 1; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 6,44e-21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 206 TYEIAPVFLLEYTLTKMR 225  
 1 TYEIAPVFLLEYTLTKMR 20

RESULT 5  
 ID DCEL\_MOUSE STANDARD: PRT: 593 AA.  
 AC P48318;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD67.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE: 94062679.  
 RA KATAROVA Z., SZABO G., MUGNAINI E., GREENSPAN R.;  
 RT "Molecular identification of the 62 kd form of glutamic acid  
 RT decarboxylase from the mouse."  
 RL Eur. J. Neurosci. 2:190-202(1990).  
 RN [2]  
 RP SEQUENCE OF 198-403 FROM N.A.  
 RC TISSUE=BRAIN;  
 RX MEDLINE: 94062679.  
 RA FAULKNER-JONES B.E., CRAM D.S., KUN J., HARRISON L.C.;  
 RT "Localization and quantitation of expression of two glutamate  
 RT decarboxylase genes in pancreatic beta-cells and other peripheral  
 RT tissues of mouse and rat."  
 RL Endocrinology 133:2962-2972(1993).  
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.  
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND  
 CC TYRDC).  
 CC -----  
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 CC -----  
 DR EMBL: Z49976; CAA90277.1; -;  
 DR EMBL: S67453; CAB32805.1; -;  
 DR MGD: MGI:95632; GAD1.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFM: PFM00282; pyridoxal\_dec; 1.  
 KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;  
 KW Pyridoxal phosphate; Multigene family;  
 FT BINDING 404  
 FT CONFLICT 234  
 FT CONFLICT 258  
 FT CONFLICT 360  
 SO SEQUENCE 593 AA; 66584 MM; 63BC57AA CRC32;

Query Match 84.5%; Score 131; DB 1; Length 593;  
 Best Local Similarity 85.0%; Pred. No. 6,98e-15;  
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAPVFLMEQITLTKMR 233  
 1 TYEIAPVFLLEYTLTKMR 20

RESULT 6  
 ID DCEL\_RAT STANDARD: PRT: 593 AA.  
 AC P18088;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)

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DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE: 9101454.
RA WYBORSKI R.J., BOND R.W., GOTTLEB D.I.;
RT "Characterization of a cDNA coding for rat glutamic acid
RT decarboxylase."
RL Brain Res. Mol. Brain Res. 8:193-198(1990).
RN [2]
RX SEQUENCE FROM N.A.
RX MEDLINE: 90132703.
RA JULIEN J.F., SAMAMA P., MALLET J.;
RT "Rat brain glutamic acid decarboxylase sequence deduced from a cloned
RT cDNA."
RL J. Neurochem. 54:703-705(1990).
RN [3]
RX SEQUENCE FROM N.A.
RX MEDLINE: 92020930.
RA MICHELSEN B.K., PETERSEN J.S., BOEL E., MOLDROP A., DYRBERG T.,
RA MADSEN O.D.;
RT "Cloning, characterization, and autoimmune recognition of rat islet
RT glutamic acid decarboxylase in insulin-dependent diabetes mellitus."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8754-8758(1991).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC -----
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CC -----
DR EMBL: M34445; AAC2037.1; -
DR EMBL: X57572; CAA40800.1; -
DR EMBL: X57573; CAA40801.1; -
DR EMBL: M76177; AAA41184.1; -
DR PIR: A41367; A41367.
DR PIR: A43756; A43756.
DR PROSITE: P500392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal_dec; 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 404 404 PYRIDOXAL PHOSPHATE (POTENTIAL).
FT CONFLICT 103 103 L -> V (IN REF. 2).
FT CONFLICT 284 284 F -> S (IN REF. 2).
FT CONFLICT 287 288 EH -> AD (IN REF. 2).
FT CONFLICT 344 345 AG -> EA (IN REF. 2).
FT CONFLICT 347 347 T -> I (IN REF. 2).
FT CONFLICT 352 353 FD -> LE (IN REF. 2).
FT CONFLICT 380 380 L -> R (IN REF. 2).
SQ SEQUENCE 593 AA; 66640 MW; 5A0B67C0 CRC32;

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Query Match 84.5%; Score 131; DB 1; Length 593;  
 Best Local Similarity 85.0%; Pred. No. 6,98e-15;  
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TYEIAPVFLMEQITLKKMR 233  
 |||||  
 QY 1 TYEIAPVFLMEYITLKKMR 20

RESULT 7

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ID DCEL_PIG STANDARD: PRT: 594 AA.
AC P48319;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)
DE (67 KD GLUTAMIC ACID DECARBOXYLASE).
GN GAD1 OR GAD67.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
RN [1]
RX SEQUENCE FROM N.A.
RX TISSUE-BRAIN;
RX MEDLINE: 95137399.
RA SUZUKI R., ASAMI N., AMANN E., WAGATSUMA M.;
RT "Sequences of two porcine glutamic acid decarboxylases (65- and
RT 67-kDa GAD)."
RL Gene 152:257-260(1995).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
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CC -----
DR EMBL: D31849; BAA06636.1; -
DR PROSITE: P500392; DDC_GAD_HDC_YDC; 1.
DR PFAM: PF00282; pyridoxal_dec; 1.
KW Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 594 AA; 66894 MW; 69D6C79C CRC32;

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Query Match 84.5%; Score 131; DB 1; Length 594;  
 Best Local Similarity 85.0%; Pred. No. 6,98e-15;  
 Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 215 TYEIAPVFLMEQITLKKMR 234  
 |||||  
 QY 1 TYEIAPVFLMEYITLKKMR 20

RESULT 8  
 ID DCEL\_HUMAN STANDARD: PRT: 594 AA.  
 AC O99259;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE GLUTAMATE DECARBOXYLASE, 67 KD ISOFORM (EC 4.1.1.15) (GAD-67)  
 DE (67 KD GLUTAMIC ACID DECARBOXYLASE).  
 GN GAD1 OR GAD.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.  
 RN [1]  
 RX SEQUENCE FROM N.A.  
 RX TISSUE-BRAIN;  
 RX MEDLINE: 92196068.  
 RA BU D.-F., ERLANDER M.G., HITZ B.C., TILAKARATNE N.J., KAUFMAN D.L.,  
 RA WAGNER-MCPHERSON C.B., EVANS G.A., TOBIN A.J.;  
 RT "Two human glutamate decarboxylases, 65-kDa GAD and 67-kDa GAD, are  
 RT each encoded by a single gene."  
 RT Proc. Natl. Acad. Sci. U.S.A. 89:2115-2119(1992).  
 RN [2]



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CC -----
DR EMBL; M18629; AAS1430.1; -.
DR PIR; A45671; A45671.
DR PIR; A46758; A46758.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM; PF00282; pyridoxal_dec; 1.
DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate; Multigene family.
FT BINDING 405 405 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 594 AA; 66824 MW; 3EC20778 CRC32;

Query Match 84.5%; Score 131; DB 1; Length 594;
Best Local Similarity 85.0%; Pred. No. 6.98e-15;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 215 TYEAPVLEVTLLKMR 234
OY 1 TYEAPVLEVTLLKMR 20

RESULT 10
ID DCE_DROME STANDARD; PRT; 510 AA.
AC P20228;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).
GN GAD OR GLB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90155291.
RA JACKSON F.R., NEWBY L.M., KULKARNI S.J.;
RT "Drosophila GABAergic systems: sequence and expression of glutamic
RT acid decarboxylase."
RL J. Neurochem. 54:1068-1078(1990).
CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
CC -1- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
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CC -----
DR EMBL; X76198; CAAS3791.1; -.
DR PIR; A30999; A30999.
DR PIR; JH0192; JH0192.
DR FLYBASE; FBgn0004516; Gad1.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFAM; PF00282; pyridoxal_dec; 1.
DR Neurotransmitter biosynthesis; Lyase; Decarboxylase;
KW Pyridoxal phosphate.
FT BINDING 322 322 PYRIDOXAL PHOSPHATE (POTENTIAL).
SQ SEQUENCE 510 AA; 57758 MW; 97C7A8F1 CRC32;

Query Match 79.4%; Score 123; DB 1; Length 510;
Best Local Similarity 75.0%; Pred. No. 6.19e-13;
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 132 TYEAPVLEVTLLKMR 151
OY 1 TYEAPVLEVTLLKMR 20

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RESULT 11
ID YC34_HELPY STANDARD; PRT; 298 AA.
AC O25832;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HYPOTHETICAL PROTEIN HP1234.
GN HP1234.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-26695 / ATCC 700392;
RX MEDLINE; 97394467.
RA TOMB J.-F., WHITE O., KERLAUGE A.R., CLAYTON R.A., SUTTON G.G.,
RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
RA LOFTUS B., RICHARDSON D., DOBSON R., KHALAK H.G., GLODER A.,
RA MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,
RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATNEY L., MALLIN E.,
RA HAYES W.S., BORDOVSKI M., KARP P.D., SMITH H.O., FRASER C.M.,
RA VENTER J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE DUF0077 (PECM) FAMILY.
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CC -----
DR EMBL; AE000628; AAD08277.1; -.
DR TIGR; HP1234; -.
DR PFAM; PF00892; DUF6; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 5 25 POTENTIAL.
FT TRANSMEM 36 56 POTENTIAL.
FT TRANSMEM 76 96 POTENTIAL.
FT TRANSMEM 97 117 POTENTIAL.
FT TRANSMEM 124 144 POTENTIAL.
FT TRANSMEM 147 167 POTENTIAL.
FT TRANSMEM 181 201 POTENTIAL.
FT TRANSMEM 216 236 POTENTIAL.
FT TRANSMEM 244 264 POTENTIAL.
FT TRANSMEM 272 292 POTENTIAL.
SQ SEQUENCE 298 AA; 32884 MW; A48B6A42 CRC32;

Query Match 47.7%; Score 74; DB 1; Length 298;
Best Local Similarity 41.2%; Pred. No. 4.19e-02;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 157 LSGTIVSLATTLDR 173
OY 4 IAPVLEVTLLKMR 20

RESULT 12
ID GBI_HELPY STANDARD; PRT; 353 AA.
AC P51876;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1), ALPHA SUBUNIT (ADENYLATE
DE CYCLASE-INHIBITING G ALPHA PROTEIN).

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OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Planorbidae; Helisoma.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-OREGON RED: TISSUE-CENTRAL GANGLION;  
RX MEDLINE: 94138304.  
RA DUGGERLIN S., BAHUS F., RICHMOND J., DOYLE R.T., LARSON D.D.,  
RA HAYDON P.G.;  
RT "Roles for arachidonic acid and GTP-binding proteins in synaptic transmission";  
RT J. Physiol. (Paris) 87:123-137(1993).  
CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.  
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).  
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.  
CC -1- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1 (G1/O/7/2)).  
-----  
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-----  
DR EMBL: L18922; AAC41538.1; -.  
DR HSSP: P10824; IAS3.  
DR PRAM: PF00503; G-alpha: 1.  
KW GTP-binding; Transducer; ADP-ribosylation; Multigene family; Myristate.  
FT INIT\_MET 0 0 BY SIMILARITY.  
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
FT NP\_BIND 39 46 GTP (BY SIMILARITY).  
FT NP\_BIND 199 202 GTP (BY SIMILARITY).  
FT NP\_BIND 268 271 GTP (BY SIMILARITY).  
FT MOD\_RES 177 177 ADP-RIBOSYL[1] (BY ACTION OF CTX) (BY SIMILARITY).  
FT MOD\_RES 350 350 ADP-RIBOSYL[1] (BY ACTION OF IAP) (BY SIMILARITY).  
SQ SEQUENCE 353 AA; 40412 MW; 6F680820 CRC32;  
-----  
Query Match 45.2%; Score 70; DB 1; Length 353;  
Best Local Similarity 35.0%; Pred. No. 2,41e-01;  
Matches 7; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
-----  
DB 294 TYEAAAYIQLOFENLNKKK 313  
QY 1 TYEIAPEVLELYVTLMKMR 20  
-----  
RESULT 13  
ID G81-LYMST STANDARD; PRT; 353 AA.  
AC P30682;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-OCT-1994 (Rel. 30, last sequence update)  
DT 15-DEC-1998 (Rel. 37, last annotation update)  
DE GUANINE NUCLEOTIDE-BINDING PROTEIN G(1), ALPHA SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN).  
OS Lymnaea stagnalis (Great pond snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Lymnaeidae; Lymnaea.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-CNS;  
RX MEDLINE: 93106153.  
RA KNOJ J.C., WEIDEMANN W., PLANTA R.J., VREUGDENHIL E.,  
RA VAN HEERIKHUIZEN H.;  
RT "Molecular cloning of G protein alpha subunits from the central nervous system of the mollusc Lymnaea stagnalis";  
RT FIBS Lett. 314:215-219(1992).

CC -1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS.  
CC -1- FUNCTION: THE G(1) PROTEINS ARE INVOLVED IN HORMONAL REGULATION OF ADENYLATE CYCLASE; THEY INHIBIT THE CYCLASE IN RESPONSE TO BETA-ADRENERGIC STIMULI.  
CC -1- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).  
CC THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.  
CC -1- SIMILARITY: BELONGS TO THE G-ALPHA FAMILY. SUBFAMILY 1 (G1/O/7/2)).  
-----  
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-----  
DR EMBL: Z15095; CAA78807.1; -.  
DR PIR: S25588; S25588.  
DR PIR: S27013; S27013.  
DR HSSP: P10824; IAS3.  
DR PRAM: PF00503; G-alpha: 1.  
KW GTP-binding; Transducer; ADP-ribosylation; Multigene family; Myristate.  
FT INIT\_MET 0 0 BY SIMILARITY.  
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
FT NP\_BIND 39 46 GTP (BY SIMILARITY).  
FT NP\_BIND 199 202 GTP (BY SIMILARITY).  
FT NP\_BIND 268 271 GTP (BY SIMILARITY).  
FT MOD\_RES 177 177 ADP-RIBOSYL[1] (BY ACTION OF CTX) (BY SIMILARITY).  
FT MOD\_RES 350 350 ADP-RIBOSYL[1] (BY ACTION OF IAP) (BY SIMILARITY).  
SQ SEQUENCE 353 AA; 40355 MW; 5CF27D61 CRC32;  
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Query Match 45.2%; Score 70; DB 1; Length 353;  
Best Local Similarity 35.0%; Pred. No. 2,41e-01;  
Matches 7; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
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DB 294 TYEAAAYIQLOFENLNKKK 313  
QY 1 TYEIAPEVLELYVTLMKMR 20  
-----  
RESULT 14  
ID REGG-BACSU STANDARD; PRT; 682 AA.  
AC O34942;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, last sequence update)  
DT 15-DEC-1998 (Rel. 37, last annotation update)  
DE ATP-DEPENDENT DNA HELICASE REGG (EC 3.6.1.-).  
GN REGG.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/staphylococcus group; Bacillus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-168;  
RA FOLGER D., ERRINGTON J.;  
RA Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: CRITICAL ROLE IN RECOMBINATION AND DNA REPAIR. HELP CATALYSING BRANCH MIGRATION. HAS A DNA UNWINDING ACTIVITY CHARACTERISTIC OF A DNA HELICASE WITH A 3' TO 5' POLARITY. REGG UNWIND BRANCHED DUPLEX DNA (Y-DNA) (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE REGG SUBFAMILY OF HELICASES.  
-----  
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(TM)  
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MPerch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Mar 7 21:51:53 2000; Maspar time 9.59 Seconds

Tabular output not generated. 144.620 Million cell updates/sec

Title: >US-08-981-824-6

Description: (1-20) from US08981824.pep

Perfect Score: 155

Sequence: 1 TYETAPVFLLEYVTLKKMR 20

Scoring table: PAM 150

Gap 15

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

sptrembl12

1:sp\_archae 2:sp\_bacteria 3:sp\_fungi 4:sp\_human

5:sp\_invertebrate 6:sp\_mammal 7:sp\_mhc 8:sp\_organelle

9:sp\_phase 10:sp\_plant 11:sp\_rodent 12:sp\_unclassified

13:sp Vertebrate 14:sp\_virus

Statistics: Mean 30.016; Variance 47.115; scale 0.637

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	153	98.7	232	13	Q93275	GLUTAMATE DECARBOXYLASE	1.56e-17
2	131	84.5	593	11	008685	67KD GLUTAMIC ACID DEC	1.18e-12
3	130	83.9	182	13	Q9W656	GLUTAMATE DECARBOXYLASE	1.95e-12
4	130	83.9	182	13	Q9W654	GLUTAMATE DECARBOXYLASE	1.95e-12
5	129	83.2	56	13	Q9W652	GLUTAMATE DECARBOXYLASE	3.22e-12
6	129	83.2	182	13	Q9W651	GLUTAMATE DECARBOXYLASE	3.22e-12
7	129	83.2	182	13	Q9W659	GLUTAMATE DECARBOXYLASE	3.22e-12
8	128	82.6	182	13	Q9W658	GLUTAMATE DECARBOXYLASE	5.29e-12
9	127	81.9	222	13	Q93276	GLUTAMATE DECARBOXYLASE	8.70e-12
10	123	79.4	563	13	Q91644	GLUTAMIC ACID DECARBOX	6.29e-11
11	121	78.1	370	5	044102	GLUTAMIC ACID DECARBOX	1.68e-10
12	121	78.1	370	5	044103	GLUTAMIC ACID DECARBOX	1.68e-10
13	111	71.6	478	11	064577	CYSTEINE SULFINIC ACID	2.11e-08
14	111	71.6	478	11	064577	CYSTEINE SULFINIC ACID	2.11e-08
15	108	69.7	267	4	Q9Y602	CYSTEINE SULFINIC ACID	8.76e-08
16	108	69.7	493	4	Q9Y600	CYSTEINE SULFINIC ACID	8.76e-08
17	105	67.7	182	13	Q9W653	GLUTAMATE DECARBOXYLASE	3.59e-07
18	105	67.7	182	13	Q9W660	GLUTAMATE DECARBOXYLASE	3.59e-07
19	104	67.1	182	13	Q9W655	GLUTAMATE DECARBOXYLASE	5.73e-07
20	104	67.1	182	13	Q9W657	GLUTAMATE DECARBOXYLASE	5.73e-07

Result ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
21	91	58.7	508	5	Q9XTP4	GLUTAMIC ACID DECARBOX	2.12e-04
22	85	54.8	180	5	Q9X411	GLUTAMATE DECARBOXYLASE	2.90e-03
23	84	54.2	375	5	Q24062	GLUTAMATE DECARBOXYLASE	4.46e-03
24	79	51.0	182	13	Q9W658	GLUTAMATE DECARBOXYLASE	3.65e-02
25	74	47.7	298	2	Q92J22	POTATIVE	2.80e-01
26	71	45.8	436	2	Q67128	HPOTHEICAL 49.7 KD P	9.15e-01
27	70	45.2	897	2	Q9XDB4	ISOLEUCY-TRNA SYNTHAS	1.35e+00
28	69	44.5	487	10	Q41760	PERMENSE 1.	1.98e+00
29	68	43.9	285	5	Q44648	K7C6.15 PROTEIN.	2.91e+00
30	68	43.9	318	11	Q921L3	DEAD PROTEIN.	2.91e+00
31	68	43.9	318	11	Q921L3	DEAD PROTEIN.	2.91e+00
32	68	43.9	586	5	Q94954	DEATH EFFECTOR DOMAIN- NSENSE-MEDIATED MRNA	2.91e+00
33	68	43.9	637	5	Q25372	ORF G.	2.91e+00
34	68	43.9	627	5	Q25294	INTEGRAL MEMBRANE PROT	2.91e+00
35	66	42.6	130	2	Q32057	Y2F PROTEIN.	6.17e+00
36	66	42.6	449	10	Q04459	F2J39.21.	6.17e+00
37	66	42.6	632	2	Q92194	POTATIVE HISTIDINE KIN	6.17e+00
38	65	41.9	298	4	Q60737	K605 PROTEIN.	8.94e+00
39	65	41.9	318	4	Q75618	F2J39.21.	8.94e+00
40	65	41.9	331	5	Q17124	F31F4.16 PROTEIN.	8.94e+00
41	65	41.9	429	5	Q26058	POTATIVE SERINE PROTEI	8.94e+00
42	65	41.9	525	11	Q9W722	ANKRYIN REPEAT-CONTAIN	8.94e+00
43	65	41.9	1070	4	Q13308	COLON CARCINOMA KINASE	8.94e+00
44	64	41.3	1956	5	Q04856	APPAP 1.	1.29e+01
45	64	41.3	3414	14	Q9WBS4	POLYPROTEIN.	1.29e+01

## ALIGNMENTS

Result ID	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	153	98.7	232	13	Q93275	GLUTAMATE DECARBOXYLASE	1.56e-17
2	131	84.5	593	11	008685	67KD GLUTAMIC ACID DEC	1.18e-12
3	130	83.9	182	13	Q9W656	GLUTAMATE DECARBOXYLASE	1.95e-12
4	130	83.9	182	13	Q9W654	GLUTAMATE DECARBOXYLASE	1.95e-12
5	129	83.2	56	13	Q9W652	GLUTAMATE DECARBOXYLASE	3.22e-12
6	129	83.2	182	13	Q9W651	GLUTAMATE DECARBOXYLASE	3.22e-12
7	129	83.2	182	13	Q9W659	GLUTAMATE DECARBOXYLASE	3.22e-12
8	128	82.6	182	13	Q9W658	GLUTAMATE DECARBOXYLASE	5.29e-12
9	127	81.9	222	13	Q93276	GLUTAMATE DECARBOXYLASE	8.70e-12
10	123	79.4	563	13	Q91644	GLUTAMIC ACID DECARBOX	6.29e-11
11	121	78.1	370	5	044102	GLUTAMIC ACID DECARBOX	1.68e-10
12	121	78.1	370	5	044103	GLUTAMIC ACID DECARBOX	1.68e-10
13	111	71.6	478	11	064577	CYSTEINE SULFINIC ACID	2.11e-08
14	111	71.6	478	11	064577	CYSTEINE SULFINIC ACID	2.11e-08
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16	108	69.7	493	4	Q9Y600	CYSTEINE SULFINIC ACID	8.76e-08
17	105	67.7	182	13	Q9W653	GLUTAMATE DECARBOXYLASE	3.59e-07
18	105	67.7	182	13	Q9W660	GLUTAMATE DECARBOXYLASE	3.59e-07
19	104	67.1	182	13	Q9W655	GLUTAMATE DECARBOXYLASE	5.73e-07
20	104	67.1	182	13	Q9W657	GLUTAMATE DECARBOXYLASE	5.73e-07

```

DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE 67MD GLUTAMIC ACID DECARBOXYLASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
RN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RP [1]
RC SEQUENCE FROM N.A.
RA STRAIN-BALB/C.
RA AUST G., STEINBRENNER H., THAMM B., ROST A.K., SEISSLER J.,
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
CC -I- CONJACOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
DR EMBL, Y12257; GAN72934.1; -.
DR PROSITE, PS00392; DDC_GAD_HDC_YDC; 1.
DR PFM; PF00282; pyridoxal_dec; 1.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 593 AA; 66648 MW; BAFE92E0 CRC32;

Query Match      84.5%; Score 131; DB 11; Length 593;
Best Local Similarity 85.0%; Pred. No. 1.18e-12;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 214 TTEIAPVFLLEYVTLKKMR 233
OY 1 TTEIAPVFLLEYVTLKKMR 20

RESULT 3
ID 09W656 PRELIMINARY; PRT; 182 AA.
AC 09W656.
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OS Coryphaenoides armatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Paracanthopterygii; Gadiformes;
OC Macrouridae; Coryphaenoides.
RP [1]
RC SEQUENCE FROM N.A.
RA TISSUE-BRAIN;
RC MEDLINE; 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RA PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
RT molecular phylogeny and evidence for a new GAD paralog."
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL, AF043267; AAD22713.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 182 AA; 19768 MW; 1225481D CRC32;

Query Match      83.9%; Score 130; DB 13; Length 182;
Best Local Similarity 94.1%; Pred. No. 1.95e-12;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 VAPVFLLEYVTLKKMR 17
OY 4 IAPVFLLEYVTLKKMR 20

RESULT 4
ID 09W654 PRELIMINARY; PRT; 182 AA.
AC 09W654.
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OC Carassius auratus (Goldfish).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinoidae; Cyprinidae; Cyprininae; Carassius.
RN [1]
RC SEQUENCE FROM N.A.
RA TISSUE-BRAIN;
RC MEDLINE; 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RA PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
RT molecular phylogeny and evidence for a new GAD paralog."
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL, AF043265; AAD22711.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 182 AA; 20097 MW; A4A23079 CRC32;

Query Match      83.9%; Score 130; DB 13; Length 182;
Best Local Similarity 94.1%; Pred. No. 1.95e-12;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 VAPVFLLEYVTLKKMR 17
OY 4 IAPVFLLEYVTLKKMR 20

RESULT 5
ID 09W662 PRELIMINARY; PRT; 56 AA.
AC 09W662.
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OS Pseudemys scripta (Slider turtle).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Testudines;
OC Cryptodira; Testudinoidea; Emydidae; Trachemys.
RP [1]
RC SEQUENCE FROM N.A.
RA TISSUE-BRAIN;
RC MEDLINE; 99261650.
RA BOSMA P.T., BLAZQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
RA PRIEDE I.G., DOCHERTY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
RT molecular phylogeny and evidence for a new GAD paralog."
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL, AF043273; AAD22719.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 56 AA; 6236 MW; 6CEA826 CRC32;

Query Match      83.2%; Score 129; DB 13; Length 56;
Best Local Similarity 94.1%; Pred. No. 3.22e-12;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 IAPVFLLEYVTLKKMR 17
OY 4 IAPVFLLEYVTLKKMR 20

RESULT 6
ID 09W661 PRELIMINARY; PRT; 182 AA.
AC 09W661.
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OS Pseudemys scripta (Slider turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;
OC Cryptodira; Testudinoidea; Emydidae; Trachemys.
RP [1]

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RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 99261650.
RA BOSMA P.T., BLAQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
PRIEDE I.G., DOCHERRY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
molecular phylogeny and evidence for a new GAD paralog."
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL; AF043272; AAC22716.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 182 AA; 19942 MW; 1699125D CRC32;

Query Match
Best Local Similarity 94.1%; Score 129; DB 13; Length 182;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 IAPVFLLEYVTLKMR 17
ID |||||
OY 4 IAPVFLLEYVTLKMR 20

RESULT 7
ID 09W659 PRELIMINARY; PRT: 182 AA.
AC 09W659;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE ISOFORM 65 (EC 4.1.1.15) (FRAGMENT).
GN GAD65.
OS Psephenia guttata (zebra finch) (Taeniopygia guttata).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
NC Neognathae; Passeriformes; Estrilidae; Estrilidae; Taeniopygia.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RX MEDLINE; 99261650.
RA BOSMA P.T., BLAQUEZ M., COLLINS M.A., BISHOP J.D.D., DROUIN G.,
PRIEDE I.G., DOCHERRY K., TRUDEAU V.L.;
RT "Multiplicity of glutamic acid decarboxylases (GAD) in vertebrates:
molecular phylogeny and evidence for a new GAD paralog."
RL Mol. Biol. Evol. 16:397-404(1999).
DR EMBL; AF043270; AAC22716.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 182 AA; 19918 MW; B67EADF CRC32;

Query Match
Best Local Similarity 94.1%; Score 129; DB 13; Length 182;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 IAPVFLLEYVTLKMR 17
ID |||||
OY 4 IAPVFLLEYVTLKMR 20

RESULT 8
ID 09Y158 PRELIMINARY; PRT: 590 AA.
AC 09Y158;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE 67.
GN GAD67.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
NC Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE LEKHORN;
RA WAGBERG F.;

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RT "Characterization of glutamate decarboxylase in chicken."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1 COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
TYRDC).
DR EMBL; AF030355; AAC01902.1; -.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
SQ SEQUENCE 590 AA; 66710 MW; 80B66DFF CRC32;

Query Match
Best Local Similarity 80.0%; Score 128; DB 13; Length 590;
Matches 16; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 211 TYETAPVFLMEQTLKMR 230
ID |||||
OY 1 TYETAPVFLMEQTLKMR 20

RESULT 9
ID 09J276 PRELIMINARY; PRT: 232 AA.
AC 09J276;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (FRAGMENT).
GN GAD67.
OS Brachydanio rerio (zebrafish) (zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
NC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 98295903.
RX MARTIN S.C., HEINRICH G., SANDELL J.H.;
RT "Sequence and expression of glutamic acid decarboxylase isoforms in
the developing zebrafish."
RL J. Comp. Neurol. 396:253-266(1998).
CC -1 COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1 SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
TYRDC).
DR EMBL; AF017265; AAC24327.1; -.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
DR PFM; PF00282; pyridoxal_dec; 1.
KW Lyase; Decarboxylase; Pyridoxal phosphate.
FT NON_TER
SQ SEQUENCE 232 AA; 25676 MW; C7DC7A63 CRC32;

Query Match
Best Local Similarity 85.0%; Score 127; DB 13; Length 232;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 2 TYETAPVFLMEQTLKMR 21
ID |||||
OY 1 TYETAPVFLMEQTLKMR 20

RESULT 10
ID 09I644 PRELIMINARY; PRT: 563 AA.
AC 09I644;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMIC ACID DECARBOXYLASE.
GN GAD.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
NC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RA WATT S.D., SPITZER N.C.;

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RL Submitted (OCT-1995) to the EMBL/Genbank/DBI databases.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).  
 DR EMBL: U38225; AAA96273.1; -.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; pyridoxal\_dec; 1.  
 DR Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 563 AA; 64095 MW; CBBH0C98 CRC32;  
 QY 185 YETIAPVFLVLEVTTLTKMR 203  
 DB 185 YETIAPVFLVLEVTTLTKMR 203  
 QY 2 YETIAPVFLVLEVTTLTKMR 20  
 RESULT 11  
 ID 044102 PRELIMINARY: PRT: 370 AA.  
 AC 044102;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).  
 GN GADI.  
 OS Drosophila pseudobscura (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA ZENG L.-W.; COMERON J.M.; CHEN B.; KREITMAN M.;  
 RL Genetic 0:0-0(1997).  
 DR EMBL: AF025807; AAB87892.1; -.  
 DR HSSP: P06543; 100D.  
 DR FLIBASE: FBgn0023295; Dpse\Gadi.  
 DR PFAM: PF00282; pyridoxal\_dec; 2.  
 FT NON\_TER 1  
 SQ SEQUENCE 370 AA; 41887 MW; A1EB456F CRC32;  
 QY 52 YETIAPVFLVLEVTTLTKMR 71  
 DB 52 YETIAPVFLVLEVTTLTKMR 71  
 QY 1 YETIAPVFLVLEVTTLTKMR 20  
 RESULT 12  
 ID 044103 PRELIMINARY: PRT: 370 AA.  
 AC 044103;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE GLUTAMIC ACID DECARBOXYLASE (FRAGMENT).  
 GN GADI.  
 OS Drosophila subobscura (Fruit fly).  
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 CC Ephydroidea; Drosophilidae; Drosophila.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA ZENG L.-W.; COMERON J.M.; CHEN B.; KREITMAN M.;  
 RL Genetic 0:0-0(1997).  
 DR EMBL: AF025808; AAB87893.1; -.  
 DR HSSP: P06543; 100C.  
 DR FLIBASE: FBgn0023244; Dsub\Gadi.  
 DR PFAM: PF00282; pyridoxal\_dec; 2.  
 FT NON\_TER 1  
 SQ SEQUENCE 370 AA; 41887 MW; A1EB456F CRC32;  
 QY 52 YETIAPVFLVLEVTTLTKMR 71  
 DB 52 YETIAPVFLVLEVTTLTKMR 71  
 QY 1 YETIAPVFLVLEVTTLTKMR 20

FT NON\_TER 370 370  
 SQ SEQUENCE 370 AA; 41923 MW; D75BDC49 CRC32;  
 Query Match  
 Best Local Similarity 78.1%; Score 121; DB 5; Length 370;  
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 DB 52 YETIAPVFLVLEVTTLTKMR 71  
 QY 1 YETIAPVFLVLEVTTLTKMR 20  
 RESULT 13  
 ID 064577 PRELIMINARY: PRT: 478 AA.  
 AC 064577;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE CYSTEINE SULFINIC ACID DECARBOXYLASE (EC 4.1.1.29)  
 DE (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-SPRAGUE-DAWLEY;  
 RC MEDLINE: 95290499.  
 RA KAIKAKIA P.J.; JERKINS A.A.; GOODSPED D.C.; STEELE R.D.;  
 RT "Cloning and characterization of rat cysteine sulfinate acid decarboxylase.";  
 RL Biochim. Biophys. Acta 1262:79-82(1995).  
 CC -1- CATALYTIC ACTIVITY: 3-SULFINO-L-ALANINE - HYPOTAURINE + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).  
 DR EMBL: M64755; AAC42063.1; -.  
 DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
 DR PFAM: PF00282; pyridoxal\_dec; 1.  
 DR Lyase; Decarboxylase; Pyridoxal phosphate.  
 SQ SEQUENCE 478 AA; 53725 MW; 4CNC0093 CRC32;  
 QY 117 YETIAPVFLVLEVTTLTKMR 136  
 DB 117 YETIAPVFLVLEVTTLTKMR 136  
 QY 1 YETIAPVFLVLEVTTLTKMR 20  
 RESULT 14  
 ID 064611 PRELIMINARY: PRT: 493 AA.  
 AC 064611;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE CYSTEINE SULFINATE DECARBOXYLASE (EC 4.1.1.29)  
 DE (SULFINOALANINE DECARBOXYLASE) (CYSTEINE-SULFINATE DECARBOXYLASE).  
 GN CSD.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE: 96283809.  
 RA REIMOND I.; SERGEANT A.; TAPPAZ M.;  
 RT "Molecular cloning and sequence analysis of the cDNA encoding rat liver cysteine sulfinate decarboxylase (CSD).";  
 RL Biochim. Biophys. Acta 1307:152-156(1996).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).

DR EMBL: X94152; CAA63858.1; -  
DR PROSITE: PS00392; DDC\_GAD\_HDC\_YDC; 1.  
DR PIRAM: PF00282; pyridoxal\_dec; 1.  
KW lyase: decarboxylase; pyridoxal phosphate.  
SQ SEQUENCE 493 AA: 55248 MW: D7A6D9A CRC32;

Query Match 71.6%; Score 111; DB 11; Length 493;  
Best Local Similarity 75.0%; Pred. No. 2.11e-08;  
Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

DB 117 TYEIAPVFVLMEEVYLKLR 136  
QY 1 TYEIAPVFVLELVTLKKMR 20

RESULT 15  
ID Q9Y602 PRELIMINARY; PRT; 267 AA.  
AC Q9Y602;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
DE CYSTEINE SULFINIC ACID DECARBOXYLASE-RELATED PROTEIN 1.  
GN CSAD.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RA PRITCHARD J.E., RAMSDEN D.B.;  
RT "Human cysteine sulfinic acid decarboxylase (CSAD)-related mRNA, 1.";  
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF16545; AAD32543.1; -  
SQ SEQUENCE 267 AA: 30264 MW: A3475A7D CRC32;

Query Match 69.7%; Score 108; DB 4; Length 267;  
Best Local Similarity 70.0%; Pred. No. 8.76e-08;  
Matches 14; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

DB 117 TYEIAPVFVLMEEVYLKLR 136  
QY 1 TYEIAPVFVLELVTLKKMR 20

Search completed: Tue Mar 7 21:52:06 2000  
Job time : 13 secs.

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